

77514

Delaval, Jan

From: Roark, Jessica
Sent: Wednesday, October 09, 2002 8:58 AM
To: Delaval, Jan
Subject: 09/780035

Jan,

Please search, including pending, for the following from 09/780035:

SEQ ID NO:70
SEQ ID NO:71.

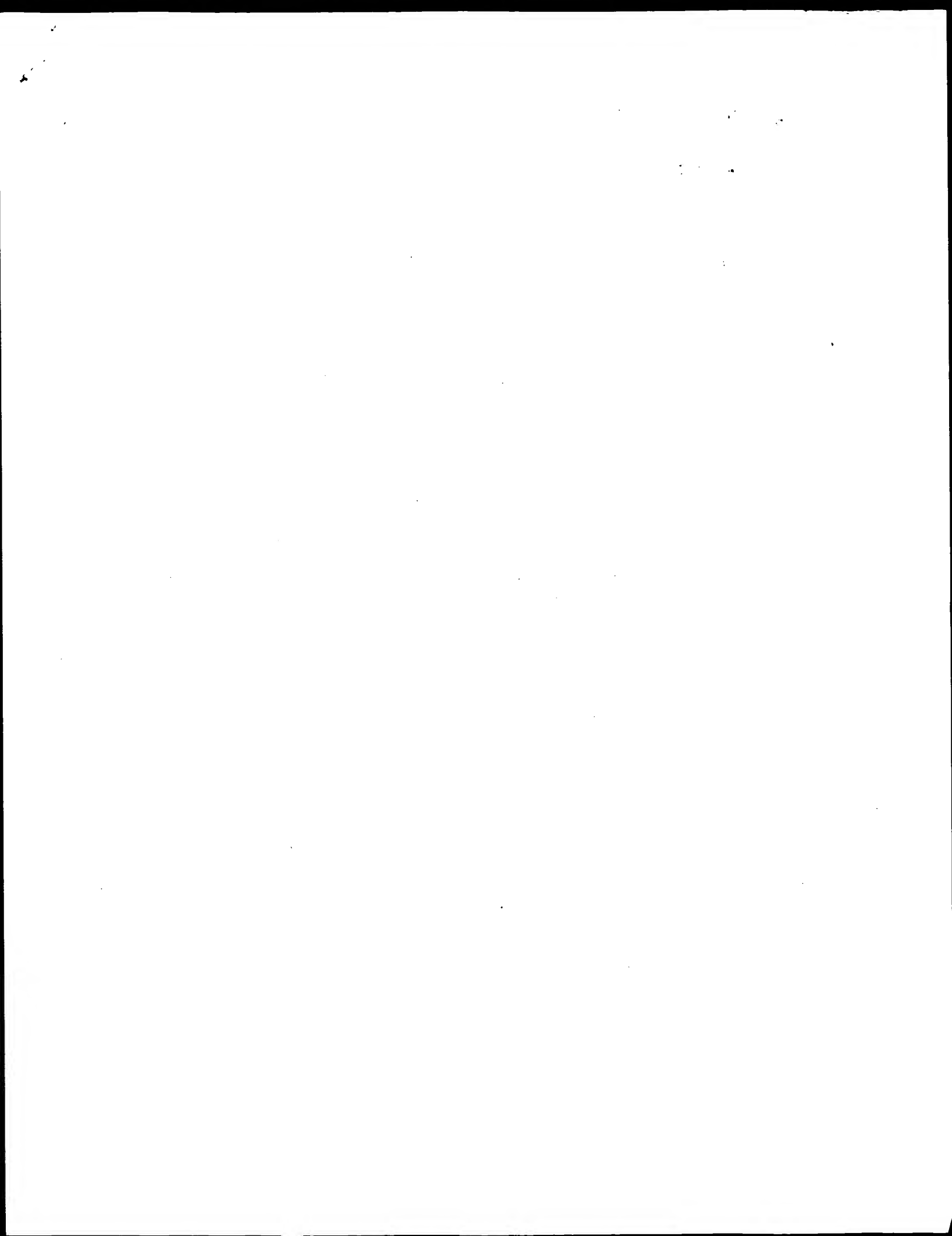
Results on paper please.

Thanks!

Jessica H. Roark

CM1 8A03
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov



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OM protein - protein search, using sw model

Run on: October 9, 2002, 09:15:09 ; Search time 84.17 Seconds

(without alignments)
87.096 Million cell updates/sec

Title: US-09-780-035-70

Perfect score: 339

Sequence: 1 YFGKLESKLVIRNLNDQVL.....FTISWKDSQPRGMATISV 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	100.0	66	22	AAG65356 Human interleukin-
2	339	100.0	157	17	AAR9564 Human interleukin-9
3	339	100.0	157	17	AAR9558 Human mature inter
4	339	100.0	157	18	AAW15701 Interferon-gamma 1
5	339	100.0	157	18	AAW24258 Human protein for
6	339	100.0	157	19	AAW77158 Human interleukin-
7	339	100.0	157	19	AAW77077 Human interleukin-
8	339	100.0	157	19	AAW77083 Human interleukin
9	339	100.0	157	19	AAW77085 Human interleukin
10	339	100.0	157	19	AAW48961 Mutant human inter
11	339	100.0	157	19	AAW48963 Mutant human inter

12	339	100.0	157	19	AAW63810 Human IL-18 protei
13	339	100.0	157	19	AAW37741 IFN-gamma inducing
14	339	100.0	157	19	AAW52176 Interferon-gamma 1
15	339	100.0	157	20	AAW39799 Interleukin-18 rec
16	339	100.0	157	21	AAW44597 Human interleukin-
17	339	100.0	157	21	AAW53904 Sequence of a matu
18	339	100.0	157	21	AAW57570 Human interleukin
19	339	100.0	157	22	AAW06661 Human interleukin-
20	339	100.0	157	22	AAW82408 Human interleukin-
21	339	100.0	157	22	AAW65294 Human interleukin-
22	339	100.0	157	22	AAW65351 Human interleukin-
23	339	100.0	158	21	AAW85167 Human interleukin-
24	339	100.0	180	19	AAW48959 Human interleukin-
25	339	100.0	193	17	AAW9560 Wild-type human in
26	339	100.0	193	18	AAW31757 Human interleukin-9
27	339	100.0	193	18	AAW22047 Interferon gamma 1
28	339	100.0	193	19	AAW77082 Interleukin 18 act
29	339	100.0	193	19	AAW37740 Interleukin-gamma 1
30	339	100.0	193	19	AAW52172 Interleukin-gamma 1
31	339	100.0	193	19	AAW47429 Interleukin-gamma 1
32	339	100.0	193	19	AAW46592 Amino acid sequenc
33	339	100.0	193	21	AAW53908 Amino acid sequenc
34	339	100.0	193	22	AAW82409 Human interleukin-
35	339	100.0	193	22	AAW30541 A human IL-18 with
36	339	100.0	193	22	AAW63830 Amino acid sequenc
37	339	97.1	193	22	AAW72608 Macaca cynomolgus
38	339	97.1	157	19	AAW77080 Human interleukin
39	339	97.1	157	19	AAW77081 Human interleukin
40	339	97.1	157	19	AAW77084 Human interleukin
41	339	97.1	157	19	AAW77086 Human interleukin
42	339	97.1	157	19	AAW77087 Human interleukin
43	339	97.1	157	19	AAW77088 Human interleukin
44	339	97.1	157	19	AAW77089 Human interleukin
45	339	97.1	157	19	AAW48962 Mutant human inter

ALIGNMENTS

RESULT	1	
AAW65356	AAW65356 standard; protein; 66 AA.	
XX	AAW65356;	
AC	30-NOV-2001 (first entry)	
XX		
DE	Human interleukin-18 (IL-18) protein N-terminal fragment.	
XX		
KW	IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;	
KW	nocotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;	
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200158956-A2.	
XX		
PD	16-AUG-2001.	
XX		
PF	09-FEB-2001; 2001WO-US04170.	
XX		
PR	10-FEB-2000; 2000US-0181608.	
XX		
PA	(BADI) BASF AG.	
XX		
PI	Ghayur T, Dixon RM, Roguska M, White M, Labkovsky B, Salfeld J;	
PI	Duncan AR, Brocklehurst SM, Mankovitch J, Shortrock CP, Thompson JE;	
PI	Lenard SN.	
XX		
DR	WPI; 2001-550020/61.	
XX		
PT	Novel antibodies and compounds capable of binding to human interleukin-18 useful for treating, e.g., inflammatory disorders,	

XX WPI: 1996-252837/26.
 DR N-PSDB: AAT32402.
 XX
 PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 XX
 PS Claim 1; Page 40; 48pp; English.
 XX
 CC A novel human protein (AAR9558) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. It enhances the cytotoxicity of
 CC killer cells and/or induces the formation of killer cells (e.g.
 CC NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
 CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
 CC high yields using host cells, esp. Escherichia coli, transformed in
 CC with a vector carrying the encoding cDNA (AAT32402). It is useful
 CC as an antiviral, antitumor, antibacterial, immunoregulatory and
 CC blood platelet enhancing agent, and can be used in adoptive
 CC immunotherapy. It is also used to raise monoclonal antibodies.
 CC
 XX A full-length sequence is given in AAR95560.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 339; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNINDOVLFIDGNRPFLFEDMTDSCRDNPRTFIITSMYKDSQPRGM 60
 Db 1 yfgklesklsvirnindovlfidggnrplfedmtsdscrdnprtlflismykdsqprgm 60
 QY 61 AVTISV 66
 Db 61 avtlsv 66

RESULT 4
 AAW15701
 ID AAW15701 standard; protein: 157 AA.
 AC AAW15701;

DT 26-JAN-1998 (first entry)
 DE Interferon-gamma inducer protein.

KW Interferon-gamma, IFN-gamma; antiviral, antineoplastic; radiotherapy;
 KW immunoregulatory; antitumor agent; chemotherapy; leukopenia;
 KW thrombocytopenia; immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.

OS Homo sapiens.

Key Location/Qualifiers
 FT Misc-difference 73 /label= Ile, Thr

PN EP767178-A1.

PD 09-APR-1997.

PF 26-SEP-1996; 96EP-0306997.

PR 20-SEP-1996; 96JP-0269105.

PR 26-SEP-1995; 95JP-0270725.

PR 29-FEB-1996; 96JP-0067434.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
 XX

DR WPI: 1997-205381/19.
 XX
 PT Human protein that induces interferon-gamma prodn. in
 PT immuno:competent cells - useful for adoptive immuno:therapy of
 PT tumours and as antimicrobial agent etc.
 XX
 PS Claim 8; Page 20; 26pp; English.

CC The present sequence represents a novel protein from human cells, which
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antineoplastic agent for antitumor
 CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukopenia and thrombocytopenia associated with
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in
 CC antitumor immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
 CC IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 CC
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 339; DB 18; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNINDOVLFIDGNRPFLFEDMTDSCRDNPRTFIITSMYKDSQPRGM 60
 Db 1 yfgklesklsvirnindovlfidggnrplfedmtsdscrdnprtlflismykdsqprgm 60
 QY 61 AVTISV 66
 Db 61 avtlsv 66

RESULT 5
 AAW24258
 ID AAW24258 standard; protein: 157 AA.
 AC AAW24258;

DT 15-OCT-1997 (first entry)

DE Human protein for induction of interferon-gamma.

KW Interferon-gamma; immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.

OS Homo sapiens.

Key Location/Qualifiers
 FT Misc-difference 73 /note= "Encoded by AYT"

PN JP09157180-A.

PD 17-JUN-1997.

PF 24-JAN-1996; 96JP-0028722.

PR 04-OCT-1995; 95JP-0279906.

PR 10-MAR-1995; 95JP-0078357.

PR 29-SEP-1995; 95JP-0274988.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI WPI: 1997-369391/34.
 DR N-PSDB: AAT80209.
 XX

PT A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases
 PS Claim 1; Page 9; 12pp; Japanese.
 XX
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX
 SQ Sequence 157 AA;
 XX
 Query Match 100.0%; Score 339; DB 18; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YFGKLESKLSVIRNLNDQVLFIDGKRPLEFDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
 1 yfgklesklsvirnlndqvlfidggnrplfedmtsdcdrdnaprtlflismykdspqrgm 60
 Db
 OY 61 AVTISV 66
 1 yfgklesklsvirnlndqvlfidggnrplfedmtsdcdrdnaprtlflismykdspqrgm 60
 61 avtlisv 66
 Db 61 avtlisv 66
 RESULT 6
 AAM77158
 ID AAM77158 standard; Protein; 157 AA.
 XX
 AC AAM77158;
 XX
 DT 26-NOV-1998 (first entry)
 XX
 DE Human Interleukin-18 protein (IL-18).
 XX
 KW Human; Interleukin-18 receptor; IL-18R; cytokine; signal transduction;
 KW immune system; treatment; autoimmune; allergic disease;
 KW immunosuppressant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73 /note= "ile or thr"
 FT
 XX
 PN EP864585-A1.
 XX
 PD 16-SEP-1998.
 XX
 PF 23-DEC-1997; 97EP-0310517.
 XX
 PR 09-OCT-1997; 97JP-0291837.
 PR 12-MAR-1997; 97JP-0074697.
 PR 28-JUL-1997; 97JP-0215488.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Okura T, Torioge K;
 XX
 DR WPI, 1998-469188/41.
 XX
 PT Interleukin-18 receptor polypeptide(s) - and corresponding DNA,
 PT which peptide compounds are useful for treating auto-immune or
 PT allergic diseases
 XX
 PS Disclosure; Pages 41-42; 51pp; English.
 XX
 CC The present sequence represents a human interleukin-18 (IL-18)
 CC polypeptide. Interleukin-18 is a type of cytokine which mediates signal
 CC transduction in immune systems. The interleukin-18 receptor polypeptide

CC can be used to neutralise interleukin-18 activity or to treat
 CC interleukin-18 receptor susceptible diseases, especially to treat
 CC auto-immune or allergic diseases or as an immunosuppressant. Conditions
 CC which may be treated include e.g. graft or organ rejection, pernicious
 CC anaemia, insulin-related diabetes, discoid lupus erythematosus,
 CC ulcerative colitis, hyperthyroidism, auto-immune hepatitis, systemic
 CC scleroderma, polymyositis, leukopenia, rheumatoid arthritis, HIV
 CC infections, asthma, atopic dermatitis, and pollinosis. The products may
 CC also be useful in the treatment of septic shock associated with
 CC IFN-alpha.
 XX
 SQ Sequence 157 AA;
 XX
 Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YFGKLESKLSVIRNLNDQVLFIDGKRPLEFDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
 1 yfgklesklsvirnlndqvlfidggnrplfedmtsdcdrdnaprtlflismykdspqrgm 60
 Db
 OY 61 AVTISV 66
 1 yfgklesklsvirnlndqvlfidggnrplfedmtsdcdrdnaprtlflismykdspqrgm 60
 61 avtlisv 66
 Db 61 avtlisv 66
 RESULT 7
 AAM77077
 ID AAM77077 standard; peptide; 157 AA.
 XX
 AC AAM77077;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE Human Interleukin 18.
 XX
 KW Human; Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
 XX
 OS Homo sapiens.
 XX
 PN EP861663-A2.
 XX
 PD 02-SEP-1998.
 XX
 PF 24-FEB-1998; 98EP-0301352.
 XX
 PR 25-FEB-1997; 97JP-0055468.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 XX
 DR WPI, 1998-448964/39.
 DR N-PSDB; AAW48226.
 XX
 PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
 PT primary hyperthyroidism and osteoporosis
 XX
 PS Claim 4; Page 18; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKISVIRNLNDQVLFIDGGRPLFEDMTSDCRDNAPRTIFITISMYKDSQPRGM 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 yfgklesklsvirnlndqvlfidggnrpplfedmtsdcrdnaprtilfifismykdsqprgm 60
 QY 61 AVTISV 66
 ||||||
 DB 61 avtlisv 66

RESULT 8

AAW77083
 ID AAW77083 standard; Peptide: 157 AA.

AC AAW77083;

DT 16-NOV-1998 (first entry)

DE Human interleukin 18 derivative 1.

Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

OS Homo sapiens.

EP861663-A2.

02-SEP-1998.

24-FEB-1998; 98EP-0301352.

25-FEB-1997; 97JP-0055468.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

WPI; 1998-448964/39.

Use of interleukin-18 to inhibit osteoclast formation - in treatment
 of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 primary hyperthyroidism and osteoporosis

Disclosure; Page 30; 56pp; English.

Interleukin-18 (IL-18) or a functional equivalent can be used for
 inhibition of osteoclast formation. IL-18 is used for treating or
 preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 osteoporosis.

Sequence 157 AA;

Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKISVIRNLNDQVLFIDGGRPLFEDMTSDCRDNAPRTIFITISMYKDSQPRGM 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 yfgklesklsvirnlndqvlfidggnrpplfedmtsdcrdnaprtilfifismykdsqprgm 60
 QY 61 AVTISV 66
 ||||||
 DB 61 avtlisv 66

RESULT 9
 AAW77085
 ID AAW77085 standard; Peptide: 157 AA.

AC AAW77085;

DT 16-NOV-1998 (first entry)

DE Human interleukin 18 derivative 3.

Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

OS Homo sapiens.

EP861663-A2.

02-SEP-1998.

24-FEB-1998; 98EP-0301352.

25-FEB-1997; 97JP-0055468.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

WPI; 1998-448964/39.

Use of interleukin-18 to inhibit osteoclast formation - in treatment
 of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 primary hyperthyroidism and osteoporosis

Disclosure; Page 31; 56pp; English.

Interleukin-18 (IL-18) or a functional equivalent can be used for
 inhibition of osteoclast formation. IL-18 is used for treating or
 preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 osteoporosis.

Sequence 157 AA;

Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKISVIRNLNDQVLFIDGGRPLFEDMTSDCRDNAPRTIFITISMYKDSQPRGM 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 yfgklesklsvirnlndqvlfidggnrpplfedmtsdcrdnaprtilfifismykdsqprgm 60
 QY 61 AVTISV 66
 ||||||
 DB 61 avtlisv 66

RESULT 10
 AAW48961
 ID AAW48961 standard; Peptide: 157 AA.

AC AAW48961;

DT 25-SEP-1998 (first entry)

DE Mutant human interferon-gamma inducing factor IGIF/MOTT2.

Interferon-gamma inducing factor; interferon-gamma; killer cell;

XX	Homo sapiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Misc-difference	68 /note= "changed from Cys in wild-type to Ser in mutant"
FT		
XX	EP845530-A2.	
PN	03-JUN-1998.	
XX		
PF	28-NOV-1997;	97EP-0309632.
XX		
PR	14-NOV-1997;	97JP-0329715.
XX	29-NOV-1996;	96JP-0333037.
PR	21-JAN-1997;	97JP-0020906.
XX		
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
XX		
PI	Kurimoto M, Okamoto I, Yamamoto K;	
XX		
DR	WPI: 1998-288747/26.	
DR	N-PSDB: AAV32625.	
XX		
PT	Mutants of interferon-gamma inducing polypeptide - useful as antitumour, antiviral, antimicrobial or anti-immunopathic agents	
XX		
PS	Claim 5; page 41; 59pp; English.	
XX		
CC	The present sequence represents the mutant human interferon-gamma inducing factor IGIF/MUT12. The wild-type human interferon-gamma factor sequence is shown in AAW48959. The invention provides for one human and mouse interferon-gamma inducing factors (IGIF) in which one or more cysteine residues are replaced with different residues at or away from the consensus sequences shown in AAW48956-M48958. The mutant IGIFs are capable of stimulating immunocompetent cells for the production of interferon-gamma and are claimed to be less toxic, more active and stable than the corresponding wild type interferon-gamma inducing factor. The mutant IGIFs are also claimed to enhance killer cell cytotoxicity and/or induce killer cell formation, and may therefore be useful as antitumour agents, antitumour immunotherapeutics, antiviral agents and antimicrobial agents. The mutant IGIFs are also claimed to be useful for treating hepatitis, acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and thrombopenia caused by radiation- and chemo-therapy.	
XX		
SQ	Sequence	157 AA:
	Query Match	100.0%; Score 339; DB 19; Length 157;
	Best Local Similarity	100.0%; Pred. No. 2.8e-33;
	Matches	66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YRGLESKLSVIRNLNDVLFITDGRKRPFLFDMTSDSCDRNAPRTIFITISMTKDSOPRCM 60	
DB	1 YRGLESKLSVIRNLNDVLFITDGRKRPFLFDMTSDSCDRNAPRTIFITISMTKDSOPRCM 60	
OY	61 AAVTISV 66	
DB	61 AAVTISV 66	
	RESULT .11	
XX	ID ' AAW48963	
AC	AAW48963;	

XX	25-SEP-1998	(first entry)	
DT			
XX			
DE	Mutant human interferon-gamma inducing factor IGIF/MUT25.		
XX			
KW	Interferon-gamma inducing factor; interferon-gamma; killer cell;		
KW	antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;		
KW	hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;		
KW	osteoporosis; thrombopenia; acquired immunodeficiency syndrome.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference	127	
FT		/note= "changed from Cys in wild-type to Ser in mutant"	
XX			
PN	EP845530-A2.		
XX			
ED	03-JUN-1998.		
XX			
PF	28-NOV-1997;	97EP-0309632.	
XX			
PR	14-NOV-1997;	97JP-0329715.	
PR	29-NOV-1996;	96JP-033037.	
PR	21-JAN-1997;	97JP-0020906.	
XX			
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.		
XX			
PI	Kurimoto M, Okamoto I, Yamamoto K;		
XX			
DR	WPI: 1998-288747/26.		
N	PSDB: AAV32627.		
XX			
PT	Mutants of interferon-gamma inducing polypeptide - useful as		
PT	antitumour, antiviral, antimicrobial or anti-immunophathic agents		
XX			
PS	Claim 5; pages 41-42; 59pp; English.		
XX			
CC	The present sequence represents the mutant human interferon-gamma		
CC	inducing factor IGIF/MUT25. The wild-type human interferon-gamma		
CC	factor sequence is shown in AAW48959. The invention provides for mutant		
CC	human and mouse interferon-gamma inducing factors (IGIF) in which one or		
CC	more cysteine residues are replaced with different residues at or away		
CC	from the consensus sequences shown in AAW48956-W48958. The mutant IGIFs		
CC	are capable of stimulating immunocompetent cells for the production of		
CC	interferon-gamma and are claimed to be less toxic, more active and		
CC	stable than the corresponding wild type interferon-gamma inducing		
CC	factor. The mutant IGIFs are also claimed to enhance killer cell		
CC	cytotoxicity and/or induce killer cell formation, and may therefore		
CC	be useful as antitumour agents, antitumour immunotherapeutics, antiviral		
CC	agents and antimicrobial agents. The mutant IGIFs are also claimed		
CC	to be useful for treating hepatitis, acquired immunodeficiency syndrome		
CC	(AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal		
CC	carcinoma), rheumatism, osteoporosis and thrombopenia caused by		
CC	radiation- and chemo-therapy.		
XX			
XX			
SQ	Sequence	157 AA:	
	Query Match	100.0%;	Score 339; DB 19; Length 157;
	Best local Similarity	100.0%;	Pred. No. 2.8e-33;
	Matches	66; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YEGKEESKLSVIRNLDQVLFIDQGRPLFEDWITSDCDNAPRTIFITISMKKDSQPRGM	60	
DB	1 YFGKLESKLSVIRNLNDQVLFIDQGRPLFEDWITSDCDNAPRTIFITISMKKDSQPRGM	60	
OY	61 AVTISV	66	
DB	61 avetisv	66	


```

RESULT 12
AAW63810
ID AAW63810 standard; protein; 157 AA.
XX
AC AAW63810;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human IL-18 protein fragment.
XX
KM Interleukin-18; IL-18; human; treatment; autoimmune disease; antibody;
KW immunosuppressant; inhibitor; receptor protein; detection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..157
FT /label= IL-18
FT /note= "partial sequence"
FT Misc-difference 73
FT /label= Thr or Ile
XX
PN EP850952-A1.
XX
PD 01-JUL-1998.
XX
PF 23-DEC-1997; 97EP-0310555.
XX
PR 28-JUL-1997; 97JP-0215490.
PR 26-DEC-1996; 96JP-0356426.
PR 21-FEB-1997; 97JP-0052526.
PR 06-JUN-1997; 97JP-0163490.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PI Kunikata T, Kurimoto M, Torigoe K, Ushio S;
XX
DR WPI: 1998-335317/30.
XX
PT New interleukin-18 receptor protein used to inhibit interleukin-18,
PT to treat autoimmune disease and as immunosuppressant - and new
PT monoclonal antibody and hybridoma used to detect interleukin-18
PT receptor protein
XX
PS Claim 5; Page 16; 35pp; English.
XX
CC This sequence represents a human interleukin-18 (IL-18) fragment which is
CC used in a method involved in neutralising IL-18 or to treat autoimmune
CC diseases or as an immunosuppressant using anti-IL-18 antibodies which
CC can inhibit IL-18. Such antibodies can also be used to detect the IL-18
CC receptor protein (labelled with an enzyme or a radioactive or fluorescent
CC substance). The protein is used to treat e.g. graft rejection, pernicious
CC anemia, atrophic gastritis, insulin-resistant diabetes, Wegener
CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
CC cold-agglutinin-related diseases, Goodpasture's syndrome, primary
CC biliary cirrhosis, symmetrical ophthalmitis, hyperthyroidism, juvenile
CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune
CC lupus erythematosus, myasthenia gravis, systemic scleroderma, systemic
CC periarthritis nodosa, multiple cold haemaglobinuria, polymyositis,
CC haemorrhagic, Basedow's disease, leukopenia, Behcet's disease, purpura
CC climactericum praecox, rheumatoid arthritis, rheumatopyra, chronic
CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic
CC nasitis, pollinosis, aptoxin-allergy and septic shock resulting from
CC production or administration of excessive gamma interferon (IFN-gamma).
XX
SQ Sequence 157 AA;

```

```

Query Match 100.0%; Score 339; DB 19; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.8e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

```

```

RESULT 13
AAW37741
ID AAW37741 standard; Protein; 157 AA.
XX
AC AAW37741;
XX
DT 07-JUL-1998 (first entry)
XX
DE IFN-gamma inducing active protein.
XX
KW Interferon-gamma inducing precursor peptide; IFN-gamma;
KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
XX
PN EP821005-A2.
XX
PD 28-JAN-1998.
XX
PF 18-JUL-1997; 97EP-0305376.
XX
PR 31-JAN-1997; 97JP-0031474.
PR 25-JUL-1996; 96JP-0213267.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PI Kurimoto M, Tanimoto T;
XX
DR WPI: 1998-088847/09.
DR N-PSDB; AAV18906.
XX
PT Conversion of interferon-inducing polypeptide precursor to active
PT polypeptide - comprises use of interferon-1-beta-converting enzyme,
PT useful for, e.g. enhancing cytotoxicity by killer cells
XX
PS Claim 5; Page 15; 18pp; English.
XX
CC This is the amino acid sequence for the interferon-gamma (IFN-gamma)
CC inducing active protein which is cleaved to form the active mature
CC protein when it is in contact with interleukin-1-beta-converting
CC enzyme (ICE). The polypeptide is used for inducing, e.g. production
CC of IFN-gamma a useful biologically active substance, enhancing
CC cytotoxicity by, and inducing the formation of killer cells. The
CC polypeptide may potentially be used as an antiviral, antitumour and
CC immunopathy agent and as an antiseptic.
XX
SQ Sequence 157 AA;

```

```

Query Match 100.0%; Score 339; DB 19; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.8e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
QY 61 AVTISV 66

```

DB 61 avl1sv 66

RESULT 14

AAW52176 standard; peptide; 157 AA.

AAW52176;

10-JUN-1998 (first entry)

Interferon-gamma inducing mature polypeptide.

Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 73 /label= Ile, Thr

EP819757-A2.

21-JAN-1998.

18-JUL-1997; 97EP-0305377.

30-MAY-1997; 97JP-0156062.

19-JUL-1997; 96JP-0207691.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Kurimoto M, Tanimoto T;

WPI; 1998-078838/08.

polypeptide-processing enzyme - for preparing mature form of

interferon-inducing polypeptide

Claim 20; Page 17; 18pp; English.

This is an interferon-gamma (IFN-gamma) inducing polypeptide sequence.

This polypeptide induces IFN-gamma production in immunocompetent cells

[the polypeptide is not named but is described in JP 27198/96 and

193098/96]. An enzyme can convert the precursor form of this polypeptide

into this active form by cleaving a linkage between Asp at amino acid

position 36 and Tyr at amino acid position 37 of the precursor. The

enzyme can be obtained from a human haematopoietic cell and can be

inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-

aspartyl-L-al. The enzyme can be used for cleaving a recombinant IFN-gamma

pro-polypeptide to form a mature polypeptide.

Sequence 157 AA;

Query Match 100.0%; Score 339; DB 19; Length 157;

Best Local Similarity 100.0%; Pred. No. 2.8e-39;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YFGKLESKLSVIRNNDQVLFIDGGRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60

1 YFGKLESKLSVIRNNDQVLFIDGGRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60

61 AVTISV 66

61 avl1sv 66

AAV39799;

29-NOV-1999 (first entry)

Interleukin-18 receptor protein sequence fragment.

Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;

IL-18 receptor sensitive disease; immune reaction; therapy.

Mammalia.

Key Location/Qualifiers

Misc-difference 73 /note= "unspecified amino acid"

JP11240898-A.

07-SEP-1999.

12-MAR-1998; 96JP-0078549.

12-MAR-1997; 97JP-0074697.

28-JUL-1997; 97JP-0215488.

09-OCT-1997; 97JP-0291837.

26-DEC-1997; 97JP-0366908.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

WPI; 1999-555071/47.

New polypeptide - useful against interleukin-18 receptor sensitive

diseases

Disclosure; Page 37; 41pp; Japanese.

This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the

invention. The IL-18R sequences were isolated from human and mouse. The

sequences can be used in drugs for treating IL-18 receptor sensitive

disease, especially effective for the relief of rejection accompanied to

organ transplantation and for the treatment and the prevention of various

diseases caused by excessive immune reaction.

Sequence 157 AA;

Query Match 100.0%; Score 339; DB 20; Length 157;

Best Local Similarity 100.0%; Pred. No. 2.8e-39;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YFGKLESKLSVIRNNDQVLFIDGGRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60

1 YFGKLESKLSVIRNNDQVLFIDGGRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60

61 AVTISV 66

61 avl1sv 66

Search completed: October 9, 2002, 11:02:44

Job time: 6455 sec

RESULT 15

AAV39799

AAV39799 standard; Protein; 157 AA.

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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:03:39 ; Search time 40.26 Seconds
(without alignments)
63.475 Million cell updates/sec

Title: US-09-780-035-70

Perfect score: 339
Sequence: 1 YFGKLESKLSVIRNLENDVLT.....FISMYKDSQPRGMATVISV 66

Scoring table:
BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	339	100.0	193	IL18_HUMAN	Q14116 homo sapien
2	277	81.7	193	IL18_HORSE	O9XSG7 equus caball
3	276	81.4	193	IL18_BOVIN	O9XU73 bos taurus
4	276	81.4	193	IL18_CANFA	O9XST0 canis famill
5	267	78.8	192	IL18_PIG	O19073 sus scrofa
6	186.5	55.0	192	IL18_MOUSE	P70380 mus musculu
7	186	54.9	194	IL18_RAT	P97636 rattus norv
8	70	20.6	1772	MSPI_PLAYO	P13828 plasmodium
9	61.5	18.1	375	YGC5_CAEEL	Q18610 caenorhabdi
10	61.5	18.1	919	RPO2_CAPVK	P16716 capripoxvir
11	61.5	18.1	950	CDAD_HUMAN	O9Y510 homo sapien
12	60.5	17.8	858	CHVA_AGRV1	P18768 agrobacteri
13	59	17.4	867	RRPO_BYDV1	P29044 barley yell
14	59	17.4	867	RRPO_BYDVR	P29045 barley yell
15	59	17.4	1507	CADE_DROME	O24298 drosophila
16	58.5	17.3	695	1	Q09740 schizosacch
17	57.5	17.0	372	1	P45333 haemophilus
18	56.5	16.7	894	YSG3_CAEEL	Q19338 caenorhabdi
19	55.5	16.4	542	RESE_BACSU	P35161 bacillus su
20	55.5	16.4	983	YOG4_CAEEL	O09499 caenorhabdi
21	55.5	16.4	1067	1	O60100 schizosacch
22	55	16.2	749	STAI_MOUSE	P42225 mus musculu
23	55	16.2	800	1	Q01819 saccharomyc
24	55	16.2	2555	1	P39847 bacillus su
25	54.5	16.1	373	LEF3_NAPO	O65365 orgyia pseu
26	54.5	16.1	669	VHRP_COMPX	P12932 compox viru
27	54	15.9	152	Y396_MYCPN	P53527 mycoplasma
28	54	15.9	321	1	P33164 burkholderi
29	54	15.9	339	YB30_ARATH	O82314 arabidopsis
30	54	15.9	375	1	P70124 mus musculu
31	54	15.9	1044	YAF3_SCHPO	O09857 schizosacch
32	54	15.9	1164	1	P17474 compox viru
33	54	15.9	1164	1	P19798 vaccinia vi

34	54	15.9	1164	1	RPO2_VARY	P33811 variola vir
35	54	15.9	1950	1	UBR1_YEAST	P19812 saccharomyc
36	53.5	15.8	317	1	YQ35_CAEEL	O09456 caenorhabdi
37	53.5	15.8	402	1	CAR1_CANPA	P32951 candida par
38	53.5	15.8	679	1	GR78_KLULA	P22010 kluyveromyc
39	53.5	15.8	700	1	NOMA_DROME	O04047 drosophila
40	53.5	15.8	1228	1	ECM_HUMAN	O13201 homo sapien
41	53	15.6	439	1	Y811_METJA	O58221 methanococ
42	53	15.6	638	1	LIK2_RAT	P53670 rattus norv
43	53	15.6	664	1	DEL1_CAEEL	O19038 caenorhabdi
44	53	15.6	714	1	CAN1_HUMAN	P07384 homo sapien
45	53	15.6	867	1	RRPO_BYDVP	P09505 barley yell

ALIGNMENTS

```

RESULT 1
ID IL18_HUMAN STANDARD; PRT; 193 AA.
AC Q14116; 075599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torisoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
in Escherichia coli, and studies on the biologic activities of the
protein."
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yong D., Guixia D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human interleukin 18 cDNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 2-193 FROM N.A.
RC TISSUE=peripheral blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DE FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
DE SUBCELLULAR LOCATION: Secreted.
DE - SIMILARITY: BELONGS TO THE IL-18 FAMILY.
DE This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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EMBL: D49950; BAA08706.1; -
EMBL: AF077611; AAC27787.1; -

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DR EMBL: AY044641; AAK95950.1;
DR EMBL: U90434; AAB50010.1;
DR MIM: 600953;
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
DR Cytokine.
KW PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F -> L (IN REF. 2).
FT CONFLICT 86 86 S -> R (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788B55 CRC64;

Query Match 100.0%; Score 339; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.6e-34;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAPRTIFIIISMKDSQPRGM 60
DB 37 YFGLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAPRTIFIIISMKDSQPRGM 96
QY 61 AVTISV 66
DB 97 AVTISV 102

RESULT 2
ID IL18_HORSE STANDARD; PRT; 193 AA.
AC O9XSO7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RX [1]
RN Nucleotide sequence from N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanle J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RA "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
-----
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-----
CC EMBL: Y11131; CAA72013.1; -.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E904ECAC CRC64;

Query Match 81.7%; Score 277; DB 1; Length 193;
Best Local Similarity 78.8%; Pred. No. 2e-26;
Matches 52; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 YFGLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAPRTIFIIISMKDSQPRGM 60
DB 37 YFGLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAPRTIFIIISMKDSQPRGM 96
QY 61 AVTISV 66
DB 97 AVTISV 102

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DB 37 YFGLEPKLSITIRNLNDQVLFIDGGRPLFEDMTSDCDRNAPRTIFIIISMKDSLTRL 96
QY 61 AVTISV 66
DB 97 AVTISV 102

RESULT 3
ID IL18_BOVIN STANDARD; PRT; 193 AA.
AC O9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RX [1]
RN Nucleotide sequence from N.A.
RA MEDLINE-20012648; PubMed-10547157;
RA Shoda I.K., Zarlega D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
-----
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-----
CC EMBL: AF124789; AAF08686.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 81.4%; Score 276; DB 1; Length 193;
Best Local Similarity 80.3%; Pred. No. 2.6e-26;
Matches 53; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 YFGLEPKLSITIRNLNDQVLFIDGGRPLFEDMTSDCDRNAPRTIFIIISMKDSQPRGM 60
DB 37 HFGLEPKLSITIRNLNDQVLFIDGGRPLFEDMTSDCDRNAPRTIFIIISMKDSLTRL 96
QY 61 AVTISV 66
DB 97 AVTISV 102

RESULT 4
ID IL18_CANFA STANDARD; PRT; 193 AA.
AC O9XSR0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

```

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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:03:04 ; Search time 105.02 Seconds

(without alignments)
108.719 Million cells updates/sec

Title: US-09-780-035-70

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....FIISMKDSQPRGMATVTSV 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	334	99.5	193	4	Q96KJ8
2	330	97.3	193	6	Q9BG15
3	276	81.4	84	6	Q95LE7
4	276	81.4	178	6	Q9WZL8
5	275	81.1	193	6	Q9GLT9
6	271	79.9	192	6	Q9SM33
7	267	78.8	192	6	Q9N1P7
8	204	60.2	45	4	Q9N049
9	155.5	45.9	196	11	Q91Z66
10	78.5	23.2	211	13	Q98S01
11	68.5	20.2	198	13	Q91R82
12	66.5	19.6	304	15	Q97685
13	65.5	19.3	1044	3	Q94173
14	64	18.9	366	16	Q66840
15	63.5	18.7	441	4	Q9HCV3
16	63	18.6	407	10	Q9C965

17	63	18.6	1766	5	Q25668
18	62	18.6	1785	5	Q25685
19	62	18.3	320	10	Q9FG29
20	61.5	18.1	1156	12	Q91MP7
21	61	18.0	1408	17	Q27557
22	60.5	17.8	718	4	Q9NVJ0
23	60.5	17.8	853	4	Q9NSG2
24	59	17.4	381	3	Q43031
25	59	17.4	532	12	Q65871
26	59	17.4	532	12	Q65876
27	59	17.4	867	12	Q91Z62
28	59	17.4	913	11	Q88195
29	59	17.4	979	11	Q91Y11
30	58.5	17.3	364	16	Q9PM33
31	58.5	17.3	419	17	Q973T1
32	58.5	17.3	713	11	Q91Y16
33	58	17.1	334	10	Q9ZSB9
34	57.5	17.0	747	3	Q42977
35	57.5	17.0	1026	3	Q74669
36	57	16.8	83	9	Q9ZX89
37	57	16.8	297	12	Q9DVT8
38	57	16.8	327	10	Q9LPT7
39	57	16.8	617	11	Q54776
40	57	16.8	638	11	Q54785
41	57	16.8	1092	3	Q9UVY2
42	56.5	16.7	98	11	Q9QWV3
43	56.5	16.7	520	5	Q21385
44	56.5	16.7	644	4	Q9Y2K1
45	56.5	16.7	647	16	Q84627

ALIGNMENTS

RESULT 1
Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.5%; Score 334; DB 4; Length 193;
Best Local Similarity 98.5%; Pred. No. 1.8e-34;
Matches 65; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFDGGRPLFEDMTDSDCRNAPRTITISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFDGGRPLFEDMTDSDCRNAPRTITISMYKDSQPRGM 96

QY 61 AVTTSV 66
DB 97 AVTTSV 102

RESULT 2
Q9BG15 PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (TREMBLrel. 17, Created)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 09:17:14 ; Search time 39.04 Seconds
(without alignments)
41.293 Million cell updates/sec

Title: US-09-780-035-70

Perfect score: 339

Sequence: 1 YFGKLESLKIVIRNLNDQVL.....FLIMYKDSQPRGMATISV 66

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5a_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5b_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5a_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5b_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/BACKFILES1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	100.0	157	2	US-08-896-605A-6
2	339	100.0	157	2	US-08-896-605A-6
3	339	100.0	157	3	US-08-884-324-1
4	339	100.0	157	3	US-08-884-324-1
5	339	100.0	157	4	US-08-996-338-26
6	339	100.0	157	4	US-08-996-338-26
7	339	100.0	157	4	US-08-974-469A-1
8	339	100.0	157	4	US-08-832-180-1
9	339	100.0	157	4	US-08-832-180-1
10	339	100.0	193	2	US-08-896-605A-2
11	339	100.0	193	2	US-08-896-605A-2
12	259	76.4	50	4	US-08-832-180-9
13	186.5	55.0	157	2	US-08-502-535B-2
14	186.5	55.0	157	2	US-08-908-005A-2
15	186.5	55.0	157	3	US-08-996-338-27
16	186.5	55.0	157	4	US-08-558-818-7
17	186.5	55.0	157	4	US-08-974-469A-7
18	186.5	55.0	157	4	US-08-832-180-8
19	186.5	55.0	157	4	US-08-832-180-8
20	186.5	55.0	157	4	US-08-832-180-11
21	186.5	55.0	157	4	US-09-253-523-2
22	71	20.9	13	4	US-09-251-911-2
23	63	18.6	13	4	US-08-832-198-4
24	55	16.2	749	2	US-08-369-796-8
25	55	16.2	749	2	US-08-852-091-8
26	55	16.2	749	2	US-08-820-754-8
27	55	16.2	749	3	US-08-956-652-8

28	55	16.2	749	3	US-08-956-869-8	Sequence 8, Appl1
29	55	16.2	749	3	US-09-012-710-7	Sequence 7, Appl1
30	55	16.2	749	3	US-08-948-547-8	Sequence 8, Appl1
31	55	16.2	749	4	US-09-556-273-7	Sequence 7, Appl1
32	55	16.2	749	4	US-08-956-653A-8	Sequence 8, Appl1
33	55	16.2	749	5	PCT-US95-17025-8	Sequence 115, App
34	54.5	16.1	616	1	US-08-453-695A-115	Sequence 115, App
35	54.5	16.1	616	1	US-08-268-161A-115	Sequence 115, App
36	54.5	16.1	616	2	US-08-453-702A-115	Sequence 115, App
37	54.5	16.1	616	4	US-09-099-639-115	Sequence 115, App
38	54.5	16.1	616	5	PCT-US95-08071-115	Sequence 115, App
39	54.5	16.1	616	4	US-09-004-838-22	Sequence 115, App
40	54.5	16.1	1366	4	US-09-004-838-88	Sequence 115, App
41	53.5	15.8	679	1	US-08-441-139-5	Sequence 115, App
42	53	15.6	119	4	US-08-680-726A-62	Sequence 8, Appl1
43	53	15.6	119	4	US-09-092-409-62	Sequence 62, Appl1
44	53	15.6	149	1	US-08-602-010A-18	Sequence 18, Appl1
45	53	15.6	149	1	US-08-680-726A-18	Sequence 18, Appl1

ALIGNMENTS

RESULT 1
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-605A-6

Query Match 100.0%; Score 339; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. NO. 5.5e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCDRNAPRITFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCDRNAPRITFIISMVKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

RESULT 2
US-08-896-501A-4
Sequence 4, Application US/08896501A

PATENT INFORMATION:
PATENT NO. 5891663
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896, 501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match 100.0%; Score 339; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.5e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCDRNAPRITFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCDRNAPRITFIISMVKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

RESULT 3
US-08-884-324-1
Sequence 1, Application US/08884324

PATENT NO. 6060283
GENERAL INFORMATION:
APPLICANT: TAKANOI OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masashi KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-884-324-1

Query Match 100.0%; Score 339; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.5e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCDRNAPRITFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCDRNAPRITFIISMVKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

RESULT 4
US-08-996-338-26
Sequence 26, Application US/08996338
PATENT NO. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takaoi
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

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OM protein - protein search, using sw model

Run on: October 9, 2002, 09:19:24 ; Search time 56.97 Seconds

(without alignments)
111.320 Million cell updates/sec

Title: US-09-780-035-70

Perfect score: 339

Sequence: 1 YFGKLESKLSYIRNLNDQVL.....FTISMWKDSQPRGMATVISV 66

Scoring table: BIOSIM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186.5	55.0	192	2	S60226 cytokine IGIF - mo
2	70	20.6	680	2	A28121 major mezozoite su
3	70	20.6	1772	2	A45532 major mezozoite su
4	64	18.9	366	1	D70351 probable hexosyltr
5	63	18.6	407	2	G96835 probable RING zinc
6	63	18.6	1785	2	A45564 major mezozoite su
7	61.5	18.1	375	2	T29568 hypothetical prote
8	61.5	18.1	919	1	RNVZCA cell surface glyco
9	61	18.0	1408	2	H69068 beta-1,2-glucan ex
10	60.5	17.8	588	1	VXAGCA beta-(1->2) glucan
11	60.5	17.8	598	2	E97686 beta-(1->2) glucan
12	60.5	17.8	598	2	AG2911 beta-(1->2) glucan
13	59	17.4	381	2	T40341 hypothetical prote
14	59	17.4	532	1	RRVOC2 RNA-directed RNA p
15	58.5	17.3	364	2	A81261 probable periplasm
16	58.5	17.3	696	2	T11674 glutamine--fructos
17	58.5	17.3	1159	2	B98198 hypothetical prote
18	58.5	17.3	1159	2	AH3088 Icmf [imported] -
19	58	17.1	334	2	T04198 hypothetical prote
20	57.5	17.0	372	2	A64176 hypothetical prote
21	57.5	17.0	747	2	T39879 hypothetical prote
22	57	16.8	327	2	T31571 hypothetical prote
23	57	16.8	617	2	JCS514 LIM motif-containi
24	57	16.8	638	2	JCS513 LIM motif-containi
25	57	16.8	906	2	AE2533 hypothetical prote
26	56.5	16.7	520	2	T16593 hypothetical prote
27	56.5	16.7	647	2	G71490 hypothetical prote
28	56.5	16.7	894	2	T20625 ABC transporter, A
29	56	16.5	318	2	H96917

30	56	16.5	381	2	T22008	hypothetical prote
31	56	16.5	595	1	TYCHRL	transforming prote
32	56	16.5	942	2	G83861	AMP-dependent DNA
33	55.5	16.4	542	2	S45557	resB protein - Bac
34	55.5	16.4	866	2	C71509	probable DNA polym
35	55.5	16.4	983	2	T19874	hypothetical prote
36	55.5	16.4	1067	2	T39449	probable importin
37	55	16.2	800	2	S29344	peptide synthetase
38	55	16.2	2555	2	C69681	phosphotesterase ho
39	54.5	16.1	278	2	H86824	metallo-beta-lacta
40	54.5	16.1	309	2	H95078	conserved hypothet
41	54.5	16.1	309	2	G97945	hypothetical prote
42	54.5	16.1	355	2	AE1661	hypothetical prote
43	54.5	16.1	355	2	AE1289	hypothetical prote
44	54.5	16.1	373	2	T10341	late expression fa
45	54.5	16.1	391	2	E69494	2-hydroxyglutaryl-

ALIGNMENTS

RESULT 1
S60226
cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OK>
A:Cross-references: EMBL:ID9949; NID:91064822; PIDN:BA08705.1; PID:91064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 55.0%; Score 186.5; DB 2; Length 192;
Best Local Similarity 58.5%; Pred. No. 8.8e-16;
Matches 38; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 2 FGLKESKLSYIRNLNDQVLFDGNGRPLFRDMDSQCRDNAPRTITISIMWKDSQPRGMA 61
DB 37 FGLRHTTAVIRNLNDQVLFVDK-RQVFEDMDTDQASAPQTRLITIMWKDSQPRGMA 95
QY 62 VTISV 66
DB 96 VTLSV 100

RESULT 2
A28121
major mezozoite surface antigen - Plasmodium yoelii (fragment)
C:Species: Plasmodium yoelii
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
R:Burns Jr., J.M.; Daly, T.M.; Vaigya, A.B.; Long, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 602-606, 1988
A:Title: The 3' portion of the gene for a Plasmodium yoelii mezozoite surface antigen
A:Reference number: A28121; MUID:88124889
A:Accession: A28121
A:Molecule type: DNA
A:Residues: 1-680 <BUR>
A:Cross-references: GB:J03612; NID:9160678; PID:9160679
A:Experimental source: strain 17XL
A:Note: The authors translated the codon GTA for residue 429 as Leu
C:Superfamily: major mezozoite surface antigen
C:Keywords: surface antigen

[illegible]

C:Superfamily: probable hexosyltransferase ytkn
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 18.9%; Score 64; DB 1; Length 366;
Best Local Similarity 29.44%; Pred. No. 4;
Matches 20; Conservative 12; Mismatches 30; Indels 6; Gaps 3;

OY 3 GKLEKLT-SVLRNLNDQVLFLFDGGRPLFEDMTSDSC----RDNAFTFIISMYSKDOP 57
| : | | | | | | | | | | | | | | | | | | | |
Db 130 GVIAKKILVSFGNGNFTDCVAVFSKIQKRLIEL-DSFCVKYIYNIGIDPDEVFSKRKL RNP 188

OY 58 RGMAYTIS 65
| : | |
Db 189 RNRILTVS 196

RESULT 5
G96835
probable RING zinc finger protein, 53384-54880 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96835
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G96835
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <STO>
A:Cross-references: GB:AE005173; NID:g6751714; PIDN:AAF27696.1; GSPDB:GN00141
C:genetics:
A:Gene: F516.15
A:Map position: 1

Query Match 18.6%; Score 63; DB 2; Length 407;
Best Local Similarity 35.8%; Pred. No. 6;
Matches 19; Conservative 9; Mismatches 17; Indels 8; Gaps 3;

OY 10 SVLRN-LNDQ-VLFLDGGRRPLFEDMTSDSCRDNAFTFIISMYSKSOPRG 59
| : | | | | | | | | | | | | | | | | | | | |
Db 5 SILVRNTLLDDQLMDHGNREHYIVITSINDEDSRSSR-----SSLDELTFQG 52

RESULT 6
A45546
major mezozoite surface antigen precursor - Plasmodium chabaudi chabaudi
C:Species: Plasmodium chabaudi chabaudi
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: A45546
R:Deleersnijder, W.; Hendrix, D.; Bendahman, N.; Hanegreets, J.; Brits, L.; Hamers-Ca
Mol. Biochem. Parasitol. 43, 231-244, 1990
A>Title: Molecular cloning and sequence analysis of the gene encoding the major mezo
A:Reference number: A45546; MUID:91218805
A:Accession: A45546
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1785
A:Cross-references: GB:M34947; NID:g160597; PID:g160598
C:Superfamily: major mezozoite surface antigen
C:Keywords: surface antigen

Query Match 18.6%; Score 63; DB 2; Length 1785;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:02:44 ; Search time 84.17 seconds

(without alignments)
44,868 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173
Sequence: 1 FLACERKRLDKLKKEDLGSRIMFTVQNEED 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.032802:*

- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	173	100.0	34	AA65457	Human interleukin-
2	173	100.0	157	AA99564	Human interferon-g
3	173	100.0	157	AA99568	Human mature inter
4	173	100.0	157	AA15701	Interferon-gamma i
5	173	100.0	157	AA24258	Human protein for-
6	173	100.0	157	AAW7158	Human interleukin-
7	173	100.0	157	AAW7207	Human interleukin-
8	173	100.0	157	AAW7080	Human interleukin-
9	173	100.0	157	AAW7083	Human interleukin
10	173	100.0	157	AAW7084	Human interleukin
11	173	100.0	157	AAW7088	Human interleukin

12	173	100.0	157	19	AAW48961	Mutant human inter
13	173	100.0	157	19	AAW48962	Mutant human inter
14	173	100.0	157	19	AAW48966	Mutant human inter
15	173	100.0	157	19	AAW63810	Human IL-18 protel
16	173	100.0	157	19	AAW37741	IFN-gamma inducing
17	173	100.0	157	19	AAW52176	Interleukin-18 rec
18	173	100.0	157	20	AAV39799	Human interleukin-
19	173	100.0	157	21	AAV44597	Human interleukin-
20	173	100.0	157	21	AAV45904	Sequence of a matu
21	173	100.0	157	21	AAV57570	Human interleukin
22	173	100.0	157	22	AAE06661	Human interleukin-
23	173	100.0	157	22	AAE82408	Human interleukin-
24	173	100.0	157	22	AAE65294	Human interleukin-
25	173	100.0	157	22	AAE65351	Human interleukin-
26	173	100.0	158	21	AAV85167	Human interleukin-
27	173	100.0	180	19	AAW48959	Human interleukin-
28	173	100.0	181	21	AAE23797	Wild-type human in
29	173	100.0	193	17	AAE9560	Human interleukin
30	173	100.0	193	18	AAW1757	Human interleukon-g
31	173	100.0	193	18	AAW22047	Interleukon gamma I
32	173	100.0	193	18	AAW7082	Interleukon gamma I
33	173	100.0	193	19	AAW37740	Interleukin 18 act
34	173	100.0	193	19	AAW52172	Interleukon-gamma i
35	173	100.0	193	19	AAW47429	Interleukon-gamma i
36	173	100.0	193	19	AAW46592	Interleukon-gamma p
37	173	100.0	193	21	AAV53908	Amino acid sequenc
38	173	100.0	193	22	AAE82409	Amino acid sequenc
39	173	100.0	193	22	AAE30541	A human IL-18 with
40	173	100.0	193	22	AAE63830	Macaca cynomolgus
41	166	96.0	193	22	AAV72608	Human interleukin
42	163	94.2	157	19	AAW7081	Human interleukin
43	163	94.2	157	19	AAW7085	Human interleukin
44	163	94.2	157	19	AAW7086	Human interleukin
45	163	94.2	157	19	AAW7087	Human interleukin

ALIGNMENTS

RESULT 1	AA65457	standard; protein; 34 AA.
ID	AA65457	
XX	AA65457	
AC	AA65457	
XX		
DT	30-NOV-2001	(first entry)
XX		
DE	Human interleukin-18 (IL-18) protein C-terminal fragment.	
KW	IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;	
KW	neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;	
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200158956-A2.	
XX		
PD	16-AUG-2001.	
XX		
PF	09-FEB-2001; 2001WO-US04170.	
XX		
PR	10-FEB-2000; 2000US-0181608.	
XX		
PA	(BAD) BASF AG.	
XX		
PI	Ghayur T, Dixon RW, Boguska M, White M, Labkovsky B, Salfeld J;	
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;	
PI	Lennard SN.	
XX		
DR	WPI; 2001-550020/61.	
XX		
PT	Novel antibodies and compounds capable of binding to human	
PT	interleukin-18 useful for treating, e.g., inflammatory disorders,	

PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -

PS Disclosure; Page 91; 91pp; English.

CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental to, a human subject suffering from,
 CC inflammatory bowel disease (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein C-terminal
 CC fragment.

CC Sequence 34 AA:

Query Match 100.0%; Score 173; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 9, 9e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLEFKLLKKEDELDGDSIMFTVQNEQ 34
 Db 1 flacekerdlfkllkkelldgdsimftvqned 34

RESULT 2
 AAR9564 ID AAR9564 standard; Protein: 157 AA.

AC AAR9564;

DT 29-SEP-1996 (first entry)

DE Human interferon-gamma inducer protein.

KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.

KW Homo sapiens.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 73 /label= Ile, Thr

FT EP712931-A2.

PD 22-MAY-1996.

PF 10-NOV-1995; 95EP-0308055.

PR 29-SEP-1995; 95JP-0274988.

PR 15-NOV-1994; 94JP-0304203.

PR 23-FEB-1995; 95JP-0058240.

PR 10-MAR-1995; 95JP-0078357.

PR 18-SEP-1995; 95JP-0262062.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
 PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
 DR WPI: 1996-252837/26.
 DR N-PSDB: AAT32411.

XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders

PS Example B-1-1; Page 28; 48pp; English.

CC A novel human protein (AAR9564) that induces interferon-gamma
 CC (IFN-gamma) prodn. by immunocompetent cells is the product of a
 CC phage cDNA clone (AAT32411) derived from a human liver library.
 CC PCR amplification of the cDNA (see also AAT32409-10) and expression
 CC in Escherichia coli XL-1 Blue MRF'kan allowed prodn. of recombinant
 CC inducer protein. This was used to construct hybridoma H-1, which
 CC produced anti-IFN-gamma inducer protein monoclonal antibody H-1mb,
 CC useful in the detection and purification of the inducer protein
 CC (see also AAR9558).

CC Sequence 157 AA:

Query Match 100.0%; Score 173; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5, 7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLEFKLLKKEDELDGDSIMFTVQNEQ 34
 Db 124 flacekerdlfkllkkelldgdsimftvqned 157

RESULT 3
 AAR9558 ID AAR9558 standard; Protein: 157 AA.

AC AAR9558;

DT 29-SEP-1996 (first entry)

DE Human mature interferon-gamma inducer protein.

KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.

KW Homo sapiens.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 73 /label= Ile, Thr

FT EP712931-A2.

PD 22-MAY-1996.

PF 10-NOV-1995; 95EP-0308055.

PR 29-SEP-1995; 95JP-0274988.

PR 15-NOV-1994; 94JP-0304203.

PR 23-FEB-1995; 95JP-0058240.

PR 10-MAR-1995; 95JP-0078357.

PR 18-SEP-1995; 95JP-0262062.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
 PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
 DR WPI: 1996-252837/26.
 DR N-PSDB: AAT32402.

PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders

PS Claim 1; Page 40; 48pp; English.
 XX A novel human protein (AAR99558) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. It enhances the cytotoxicity of
 CC killer cells and/or induces the formation of killer cells (e.g.
 CC NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
 CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
 CC high yields using host cells, esp. Escherichia coli, transformed
 CC with a vector carrying the encoding cDNA (AAR32402). It is useful
 CC as an antiviral, antitumor, antibacterial, immunoregulatory and
 CC blood platelet enhancing agent, and can be used in adoptive
 CC immunotherapy. It is also used to raise monoclonal antibodies.
 CC A full-length sequence is given in AAR99560.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 173; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACEKERDLFKLIKKEDELGRSIMPYONED 34
 Db 124 flacekerdlfklikkedelgrsimftvqned 157

RESULT 4
 AAM15701
 ID AAM15701 standard; protein; 157 AA.

AC AAM15701;

DT 26-JAN-1998 (first entry)

DE Interferon-gamma inducer protein.

KM Interferon-gamma, IFN-gamma; antiviral; antineoplastic; radiotherapy;
 immunoregulatory; antitumor agent; chemotherapy; leukopenia;

KW thrombocytopenia; immunocompetent cell; asthma; hayfever;
 rheumatism; interleukin; killer cell.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 73 /label= Ile, Thr

XX EP67178-A1.

XX 09-APR-1997.

XX 26-SEP-1996; 96EP-0306997.

XX 20-SEP-1996; 96DP-0269105.

XX 26-SEP-1995; 95JP-0270725.

XX 29-FEB-1996; 96JP-0067434.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Arita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
 DR WPI; 1997-205381/19.

XX Human protein that induces interferon-gamma prodn. in
 PT immuno-competent cells - useful for adoptive immuno-therapy of
 PT tumours and as antimicrobial agent etc.

XX Claim 8; Page 20; 26pp; English.

XX The present sequence represents a novel protein from human cells, which
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antineoplastic agent for antitumour

CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukopenia and thrombocytopenia associated with
 CC radiotherapy or chemotherapy of leukemia and other cancers. When used in
 CC antitumor immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
 CC IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 173; DB 18; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACEKERDLFKLIKKEDELGRSIMPYONED 34
 Db 124 flacekerdlfklikkedelgrsimftvqned 157

RESULT 5
 AAM24258
 ID AAM24258 standard; Protein; 157 AA.

AC AAM24258;

DT 15-OCT-1997 (first entry)

DE Human protein for induction of interferon-gamma.

KM Interferon-gamma; immunocompetent cell; malignant tumour;
 viral disease; bacterial infection; immune disease.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 73 /note= "Encoded by AYT"

XX JP09157180-A.

XX 17-JUN-1997.

XX 24-JAN-1996; 96JP-0028722.

XX 04-OCT-1995; 95JP-0279906.

XX 10-MAR-1995; 95JP-0078357.

XX 29-SEP-1995; 95JP-0274988.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX WPI; 1997-369391/34.

XX N-PSDB; AAT80209.

XX A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases

XX Claim 1; Page 9; 12pp; Japanese.

XX This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.

XX Sequence 157 AA;

Query Match 100.0%; Score 173; DB 18; Length 157;

Best Local Similarity 100.0%; Pred. No. 5.7e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACKEKRDLEFKLLKKEDELGDRSIMFTVQNEED 34
124 flacekerdlfkllkkelldgdrsimftvqned 157

RESULT 6

AAW77158
ID AAW77158 standard; Protein; 157 AA.

XX AAW77158;

DT 26-NOV-1998 (first entry)

DE Human Interleukin-18 protein (IL-18).

XX Human; Interleukin-18 receptor; IL-18R; cytokine; signal transduction;

KW immune system; treatment; autoimmune; allergic disease;

KM immunosuppressant.

XX Homo sapiens.

OS Homo sapiens.

PH Key Location/Qualifiers

FT MISC-difference 73 /note="Ile or Thr"

XX EP864585-A1.

PD 16-SEP-1998.

XX 23-DEC-1997; 97EP-0310517.

XX 09-OCT-1997; 97JP-0291837.

PR 12-MAR-1997; 97JP-0074697.

PR 28-JUL-1997; 97JP-0215488.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kurimoto M, Okura T, Torioge K;

XX WPI; 1998-469188/41.

DR Interleukin-18 receptor polypeptide(s) - and corresponding DNA,

XX which peptide compounds are useful for treating auto-immune or

XX allergic diseases

XX Disclosure; Pages 41-42; 51pp; English.

XX The present sequence represents a human interleukin-18 (IL-18)

XX polypeptide. Interleukin-18 is a type of cytokine which mediates signal

XX transduction in immune systems. The interleukin-18 receptor polypeptide

XX can be used to neutralise interleukin-18 activity or to treat

XX interleukin-18 receptor susceptible diseases, especially to treat

XX autoimmune or allergic diseases or as an immunosuppressant. Conditions

XX anemia, insulin-related diabetes, discoid lupus erythematosus,

XX ulcerative colitis, hyperthyroidism, autoimmune hepatitis, systemic

XX scleroderma, polymyositis, leukopenia, rheumatoid arthritis, HIV

XX infections, asthma, atopic dermatitis, and pollinosis. The products may

XX also be useful in the treatment of septic shock associated with

DB 124 flacekerdlfkllkkelldgdrsimftvqned 157

RESULT 7

AAW77077
ID AAW77077 standard; peptide; 157 AA.

XX AAW77077;

DT 16-NOV-1998 (first entry)

DE Human Interleukin 18.

XX Human; Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KM chronic rheumatoid arthritis; deformity ositits; primary hyperthyroidism.

XX Homo sapiens.

XX EP861663-A2.

PD 02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI; 1998-448964/39.

XX N-PSDB; AAV48226.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment

XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,

XX osteosarcoma, chronic rheumatoid arthritis, deformity ositits,

XX primary hyperthyroidism and osteoporosis

XX Claim 4; Page 18; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for

XX inhibition of osteoclast formation. IL-18 is used for treating or

XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma

XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid

XX arthritis, deformity ositits, primary hyperthyroidism, osteopenia and

XX osteoporosis.

XX Sequence 157 AA;

XX Query Match 100.0%; Score 173; DB 19; Length 157;

XX Best Local Similarity 100.0%; Pred. No. 5.7e-18;

XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 FLACKEKRDLEFKLLKKEDELGDRSIMFTVQNEED 34

XX 124 flacekerdlfkllkkelldgdrsimftvqned 157

XX RESULT 8

XX AAW77080
ID AAW77080 standard; Peptide; 157 AA.

XX AAW77080;

XX 16-NOV-1998 (first entry)

XX Human Interleukin 18 mutant protein.

* XX	Homo sapiens.
OS XX	
FH FT	Key Location/Qualifiers
FT	misc_difference 38 /note= "Cysteine residue replaced with a serine residue"
FT	misc_difference 68 /note= "Cysteine residue replaced with a serine residue"
FT	misc_difference 76 /note= "Cysteine residue replaced with an alanine residue"
FT FT	
XX XX	EP861663-A2.
XX PD	02-SEP-1998.
XX PF	24-FEB-1998; 98EP-0301352.
XX PR	25-FEB-1997; 97JP-0055468.
XX PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI	Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N:
XX DR	WPL: 1998-448964/39.
DR N-PSDB:	AAV48229.
PT	Use of interleukin-18 to inhibit osteoclast formation - in treatment
PT	of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
PT	osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
PI	primary hyperthyroidism and osteoporosis
XX PS	Disclosure; Page 22; 56pp; English.
XX CC	Interleukin-18 (IL-18) or a functional equivalent can be used for
CC	inhibition of osteoclast formation. IL-18 is used for treating or
CC	preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC	Behcet's syndrome, osteosarcoma, arthropathy, Chronic Rheumatoid
CC	arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
CC	osteoporosis.
SQ	Sequence 157 AA:
OY	Query Match 100.0%; Score 173; DB 19; Length 157;
	Best Local Similarity 100.0%; Pred. No. 5.7e-18;
	Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 FLACKEKRDLFKLILKKEDLGDRSIMPVONED 34 124 flacekerdflkllkkedelgdrsimftvqned 157
RESULT 9	
ID AAM77083	AAW77083 standard; Peptide: 157 AA.
XX AC AAW77083;	
DT DT	16-NOV-1998 (first entry)
XX DE	Human Interleukin 18 derivative 1.
XX KW	Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KM	osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX OS	chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
XX PN	Homo sapiens.
PD EP861663-A2.	
PD	02-SEP-1998.

PF	24-FEB-1998:	98EP-0301352.
XX		
PR	25-FEB-1997:	97JP-0055468.
XX		
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
XX		
PI	Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;	
XX		
DR	WPI; 1998-448964/39.	
XX		
PT	Use of interleukin-18 to inhibit osteoclast formation - in treatment	
PT	of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome.	
PT	osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,	
PT	primary hyperthyroidism and osteoporosis	
XX		
PS	Disclosure: Page 30; 56pp; English.	
XX		
CC	Interleukin-18 (IL-18) or a functional equivalent can be used for	
CC	inhibition of osteoclast formation. IL-18 is used for treating or	
CC	preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma	
CC	Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid	
CC	arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and	
CC	osteoporosis.	
XX		
XX		
Sequence	157 AA;	
50		

Query Match:	100.0%;	Score 173;	DB 19;	Length 157;
Best Local Similarity:	100.0%;	Pred. NO. 5.7e-18;		
Matches 34;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
1	FLACEKERDLFKLILKEDELGDRSIMPTVQNE	34		
Db	124	flacekerdlfkllkkedelgdrsimftveqned	157	
RESULT 10				
ID	AAW77084	standard; Peptide; 157 AA.		
XX	AAW77084			
XX	AAW77084;			
XX	16-NOV-1998	(first entry)		
XX	Human interleukin 18 derivative 2.			
DE	Human: interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;			
KW	osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;			
KM	chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.			
XX				
OS	Homo sapiens.			
XX				
PN	EP861663-A2.			
XX				
PD	02-SEP-1998.			
XX				
PF	24-FEB-1998; 98EP-0301352.			
XX				
PR	25-FEB-1997; 97JP-0055468.			
XX				
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.			
XX				
PI	Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;			
XX				
DR	WPI; 1998-448964/39.			
XX				
PT	Use of interleukin-18 to inhibit osteoclast formation - in treatment			
PT	of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,			
PT	osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,			
XX	primary hyperthyroidism and osteoporosis			
XX				
XX	Disclosure; Page 30-31; 56pp; English.			

CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA:

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 34
 |||||
 DB 124 flacekerdlfkllkkelgdrsimftvqned 157

RESULT 11

AAW77088 standard; Peptide: 157 AA.

AAW77088;

16-NOV-1998 (first entry)

Human interleukin 18 derivative 6.

Human; Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

Homo sapiens.

EP861663-A2.

02-SEP-1998.

24-FEB-1998; 98EP-0301352.

25-FEB-1997; 97JP-0055468.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

WPI: 1998-448964/39.

Use of interleukin-18 to inhibit osteoclast formation - in treatment
 of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 primary hyperthyroidism and osteoporosis

Disclosure: Page 33; 56pp; English.

Interleukin-18 (IL-18) or a functional equivalent can be used for
 inhibition of osteoclast formation. IL-18 is used for treating or
 preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 osteoporosis.

Sequence 157 AA:

Query Match 100.0%; Score 173; DB 19; Length 157;

Best Local Similarity 100.0%; Pred. No. 5.7e-18;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 34
 |||||
 DB 124 flacekerdlfkllkkelgdrsimftvqned 157

RESULT 12

AAW48961 standard; Peptide: 157 AA.

AAW48961;

25-SEP-1998 (first entry)

Mutant human interferon-gamma inducing factor IGIF/MUT12.

Interferon-gamma inducing factor; interferon-gamma; killer cell;
 antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 osteoporosis; thrombopenia; acquired immunodeficiency syndrome.

Homo sapiens.

Synthetic.

EP845530-A2.

03-JUN-1998.

28-NOV-1997; 97EP-0309632.

14-NOV-1997; 97JP-0329715.

29-NOV-1996; 96JP-0333037.

21-JAN-1997; 97JP-0020906.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Kurimoto M, Okamoto I, Yamamoto K;

WPI: 1998-288747/26.

N-PSDB: AAV32625.

Mutants of interferon-gamma inducing polypeptide - useful as
 antitumour, antiviral, antimicrobial or anti-immunopathic agents
 Claim 5; page 41; 59pp; English.

The present sequence represents the mutant human interferon-gamma
 inducing factor IGIF/MUT12. The wild-type human interferon-gamma
 factor sequence is shown in AAW48959. The invention provides for mutant
 human and mouse interferon-gamma inducing factors (IGIF) in which one
 or more cysteine residues are replaced with different residues at or
 away from the consensus sequences shown in AAW48956-AA48958. The mutant
 IGIFs are capable of stimulating immunocompetent cells for the production
 of interferon-gamma and are claimed to be less toxic, more active and
 stable than the corresponding wild type interferon-gamma inducing
 factor. The mutant IGIFs are also claimed to enhance killer cell
 cytotoxicity and/or induce killer cell formation, and may therefore
 be useful as antitumour agents, antitumour immunotherapeutics, antiviral
 agents and antimicrobial agents. The mutant IGIFs are also claimed
 to be useful for treating hepatitis, acquired immunodeficiency syndrome
 (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
 carcinoma), rheumatism, osteoporosis and thrombopenia caused by
 radiation- and chemo-therapy.

Sequence 157 AA:

Query Match 100.0%; Score 173; DB 19; Length 157;

Best Local Similarity 100.0%; Pred. No. 5.7e-18;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 34

Db 124 flacekerdflkllkdelgdrsimftvqned 157

RESULT 13

AAW48962

ID AAW48962 standard; Peptide: 157 AA.

AC AAW48962;

DT 25-SEP-1998 (first entry)

DE Mutant human interferon-gamma inducing factor IGIF/MUT21.

KW Interferon-gamma inducing factor; Interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 38 /note="changed from Cys in wild-type to Ser in
 mutant"

EP845530-A2.

03-JUN-1998.

28-NOV-1997; 97EP-0309632.

14-NOV-1997; 97JP-0329715.

29-NOV-1996; 96JP-0333037.

21-JAN-1997; 97JP-0020906.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Kurimoto M, Okamoto I, Yamamoto K;

WPI; 1998-288747/26.

N-PSDB; AAV32626.

PT Mutants of interferon-gamma inducing polypeptide - useful as
 antitumour, antiviral, antimicrobial or anti-immunopathic agents
 Claim 5; page 41; 59pp; English.

CC The present sequence represents the mutant human interferon-gamma
 CC inducing factor IGIF/MUT21. The wild-type human interferon-gamma
 CC factor sequence is shown in AAW48959. The invention provides for mutant
 CC human and mouse interferon-gamma inducing factors (IGIF) in which one or
 CC more cysteine residues are replaced with different residues at or away
 CC from the consensus sequences shown in AAW48956-W48958. The mutant IGIFs
 CC are capable of stimulating immunocompetent cells for the production of
 CC interferon-gamma and are claimed to be less toxic, more active and
 CC stable than the corresponding wild type interferon-gamma inducing
 CC factor. The mutant IGIFs are also claimed to enhance killer cell
 CC cytotoxicity and/or induce killer cell formation, and may therefore
 CC be useful as antitumour agents, antitumour immunotherapeutics, antiviral
 CC agents and antimicrobial agents. The mutant IGIFs are also claimed
 CC to be useful for treating hepatitis, acquired immunodeficiency syndrome
 CC (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
 CC carcinoma), rheumatism, osteoporosis and thrombopenia caused by
 CC radiation- and chemo-therapy.

Sequence 157 AA;

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLACEKERDLPKLLKKEDELGDRSIMFTVQNEED 34
 Db 124 flacekerdflkllkdelgdrsimftvqned 157

RESULT 14

AAW48966

ID AAW48966 standard; Peptide: 157 AA.

AC AAW48966;

DT 25-SEP-1998 (first entry)

DE Mutant human interferon-gamma inducing factor IGIF/MUT35.

KW Interferon-gamma inducing factor; Interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 38 /note="changed from Cys in wild-type to Ser in
 mutant"
 FT Misc-difference 76 /note="changed from Cys in wild-type to Ala in
 mutant"

EP845530-A2.

03-JUN-1998.

28-NOV-1997; 97EP-0309632.

14-NOV-1997; 97JP-0329715.

29-NOV-1996; 96JP-0333037.

21-JAN-1997; 97JP-0020906.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Kurimoto M, Okamoto I, Yamamoto K;

WPI; 1998-288747/26.

N-PSDB; AAV32630.

PT Mutants of interferon-gamma inducing polypeptide - useful as
 antitumour, antiviral, antimicrobial or anti-immunopathic agents
 Claim 5; page 43; 59pp; English.

CC The present sequence represents the mutant human interferon-gamma
 CC inducing factor IGIF/MUT35. The wild-type human interferon-gamma
 CC factor (IGIF) sequence is shown in AAW48959. The invention provides for
 CC mutant human and mouse interferon-gamma inducing factors in which one
 CC or more cysteine residues are replaced with different residues at or
 CC away from the consensus sequences shown in AAW48956-W48958. The mutant
 CC IGIFs are capable of stimulating immunocompetent cells for the production
 CC of interferon-gamma and are claimed to be less toxic, more active and
 CC stable than the corresponding wild type IGIF. The mutant IGIFs are also
 CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
 CC formation, and may therefore be useful as antitumour agents, antitumour
 CC immunotherapeutics, antiviral agents and antimicrobial agents. The
 CC mutant IGIFs are also claimed to be useful for treating hepatitis,
 CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
 CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
 CC thrombopenia caused by radiation- and chemo-therapy.

Sequence 157 AA;

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTYQNE D 34
 Db 124 flacekerdlfkllkkelgdrsimftvqned 157

RESULT 15

AAW63810
 ID AAW63810 standard; protein; 157 AA.

XX AAW63810;

XX 28-SEP-1998 (first entry)

XX Human IL-18 protein fragment.

XX Interleukin-18: IL-18; human; treatment; autoimmune disease; antibody;

XX immunosuppressant; inhibitor; receptor protein; detection.

XX Homo sapiens.

XX key Location/Qualifiers

FT Protein

FT 1..157

FT /label= IL-18

FT /note= "partial sequence"

FT Misc-difference 73

FT /label= Thr or Ile

XX EP850952-A1.

XX 01-JUL-1998.

XX 23-DEC-1997; 97EP-0310555.

XX 28-JUL-1997; 97JP-0215490.

XX 26-DEC-1996; 96JP-0356426.

XX 21-FEB-1997; 97JP-0052526.

XX 06-JUN-1997; 97JP-0163490.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kunikata T, Kurimoto M, Torigoe K, Ushio S;

XX WPI: 1998-335317/30.

XX New Interleukin-18 receptor protein used to inhibit interleukin-18,
 PT to treat autoimmune disease and as immunosuppressant - and new
 PT monoclonal antibody and hybridoma used to detect interleukin-18
 PT receptor protein

XX Claim 5; Page 16; 35pp; English.

XX This sequence represents a human interleukin-18 (IL-18) fragment which is
 CC used in a method involved in neutralising IL-18 or to treat autoimmune
 CC diseases or as an immunosuppressant using anti-IL-18 antibodies which
 CC can inhibit IL-18. Such antibodies can also be used to detect the IL-18
 CC receptor protein (labelled with an enzyme or a radioactive or fluorescent
 CC substance). The protein is used to treat e.g. graft rejection, pernicious
 CC anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener
 CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
 CC cold-agglutinin-related diseases, Goodpasture's syndrome, primary
 CC biliary cirrhosis, symphetic ophthalmitis, hyperthyroidism, juvenile
 CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune
 CC haemolytic anaemia, myasthenia gravis, systemic scleroderma, systemic
 CC lupus erythematosus, polyepic cold haemaglobinuria, polymyositis,
 CC periarthritis nodosa, multiple sclerosis, Addison's disease, purpura
 CC haemorrhagica, Basedow's disease, leukopenia, Behcet's disease,
 CC * clmacacterium praecox, rheumatoid arthritis, rheumatopyra, chronic
 CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic

CC naititis, pollinosis, aptioxin-allergy and septic shock resulting from
 CC production or administration of excessive gamma interferon (IFN-gamma).
 CC XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTYQNE D 34
 Db 124 flacekerdlfkllkkelgdrsimftvqned 157

Search completed: October 9, 2002, 11:02:44
 Job time: 6455 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:04:48 ; Search time 56.97 Seconds
(Without alignments)
57.347 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173

Sequence: 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNE 34

Scoring table: BLOSUM62

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	71.1	192	2	cytokine IGIF - mo
2	58	33.5	499	2	monomine oxidase
3	53.5	30.9	1359	2	hypothetical prote
4	53	30.6	259	1	site-specific DNA
5	53	30.6	730	2	fasciclin IV precu
6	52.5	30.3	356	2	hypothetical prote
7	52	30.1	217	2	two component resp
8	52	30.1	262	2	hypothetical prote
9	52	30.1	1277	2	hypothetical prote
10	51.5	29.8	429	2	enolase (imported)
11	51.5	29.8	432	2	phosphorylase hy
12	51.5	29.8	1119	2	nuclear matrix con
13	51.5	29.8	2262	2	large protein L -
14	51	29.5	307	2	catechol 2,3-dioxy
15	51	29.5	307	4	catechol 2,3-dioxy
16	51	29.5	339	2	hypothetical prote
17	51	29.5	354	2	response regulator
18	51	29.5	357	2	hypothetical prote
19	51	29.5	431	2	conserved hypotet
20	50.5	29.2	384	2	probable N-acetyl
21	50	28.9	195	2	hypothetical prote
22	50	28.9	258	2	flagellar export p
23	50	28.9	258	2	probable flagellar
24	50	28.9	314	2	catechol 2,3-dioxy
25	50	28.9	643	2	probable transcrip
26	50	28.9	3944	2	hypothetical prote
27	49.5	28.6	231	2	DNA repair/recomb
28	49	28.3	94	1	h-100 protein alph
29	49	28.3	186	2	hypothetical prote

30	49	28.3	307	2	JC2503	catechol 2,3-dioxy
31	49	28.3	307	2	JC4885	catechol 2,3-dioxy
32	49	28.3	399	2	EA4964	hypothetical prote
33	49	28.3	407	2	AE1073	phosphopentomutase
34	49	28.3	420	2	T02363	hypothetical prote
35	49	28.3	440	2	F70117	hypothetical prote
36	49	28.3	1195	2	S38174	probable purine nu
37	49	28.3	1459	2	S50437	hypothetical prote
38	48.5	28.0	124	2	A64391	hypothetical prote
39	48.5	28.0	475	1	A56824	diacylglycerol phosphatase
40	48.5	28.0	1004	2	H81683	helicase, probable
41	48.5	28.0	1036	2	E96682	hypothetical prote
42	48	27.7	146	2	T16561	hypothetical prote
43	48	27.7	150	2	S01770	Spec2a protein - s
44	48	27.7	190	2	J01790	Salp15k protein - s
45	48	27.7	238	2	C82884	conserved hypotet

ALIGNMENTS

RESULT 1
S60226
cytokine IGIF - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C/Accession: S60226
R/Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995
A>Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A/Reference number: S60226; MUID:96061009
A/Accession: S60226
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-192 <OKA>
A/Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823
C/Superfamily: Mus musculus cytokine IGIF

Query Match 71.1%; Score 123; DB 2; Length 192;
Best Local Similarity 71.9%; Pred. No. 1.8e-09;
Matches 23; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNE 32
DB 157 FLACQKEDDAFLKLLKKEDELGDRSIMFTVQNE 188

RESULT 2
I51346
monomine oxidase - rainbow trout

C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C/Accession: I51346
R/Chen, K.; Wu, H.F.; Grimsby, J.; Shih, J.C.
Mol. Pharmacol. 46, 1226-1233, 1994
A>Title: Cloning of a novel monomine oxidase cDNA from trout liver.
A/Reference number: I51346; MUID:95107295
A/Accession: I51346
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-499 <CHE>
A/Cross-references: GB:L37876; NID:g728484; PIDN:AAA64302.1; PID:g728485
C/Genetics:

A/Name: MAO

Query Match 33.5%; Score 58; DB 2; Length 499;
Best Local Similarity 46.4%; Pred. No. 4.2;
Matches 13; Conservative 6; Mismatches 7; Indels 2; Gaps 1;
QY 6 KERDLFKLLKKEDELGDRSIMFTVQNE 33

Db 26 KEGSLPVLLEARDRVGRT--FTYQNE 51

RESULT 3

T34036
hypothetical protein B0041.7 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T34036

R:Fulton, R.; Wohldmann, P.

submitted to the EMBL Data Library, April 1997

A:Description: The sequence of *C. elegans* cosmid B0041.

A:Reference number: 221466

A:Accession: T34036

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1359 <FUL>

A:Cross-references: EMBL:AF000196; PIDN:AA24256.1; GSPDB:GN00019; CESP:B0041.7

A:Experimental source: strain Bristol N2; clone B0041

C:Genetics:

A:Gene: CESP:B0041.7

A:Map position: 1

A:Introns: 12/2; 59/2; 248/2; 582/1; 675/1; 733/3; 966/2; 1044/2; 1310/3

Query Match

Best Local Similarity 30.9%; Score 53.5; DB 2; Length 1359;

Matches 13; Conservative 9; Mismatches 6; Indels 9; Gaps 1;

OY 2 LACEKERDLFKL-----TLKKEDELGDRSIMFT 29

Db 934 LVKEEDRDFFALSKRLILVELIKKECEIGDKLWFS 970

RESULT 4

site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) - phage T2

C:Species: phage T2

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 05-May-2000

C:Accession: A30195

R:Miner, Z.; Hattman, S.

J. Bacteriol. 170, 5177-5184, 1988

A:Title: Molecular cloning, sequencing, and mapping of the bacteriophage T2 dam gene.

A:Reference number: A30195; MUID:89033901

A:Accession: A30195

A:Molecule type: DNA

A:Residues: 1-259 <MIN>

A:Cross-references: GB:M22342; NID:g215792; PIDN:AAA32477.1; PID:g215793

C:Genetics:

A:Gene: dam

C:Superfamily: site-specific methyltransferase (adenine-specific) EcoRV

C:Keywords: methyltransferase; S-adenosylmethionine

Query Match

Best Local Similarity 30.6%; Score 53; DB 1; Length 259;

Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

OY 1 FLACEKERDLFKLILKKEDELGDRSIMFTYON 32

Db 184 FWSEBEKDLNML-----DSLMDRGIKRGLSN 211

RESULT 5

fasciclin IV precursor - American bird grasshopper

C:Species: *Schistocerca americana* (American bird grasshopper)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: JH0798

R:Kolodkin, A.; Mathes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good

Neuron 9, 831-845, 1992

A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in

A:Reference number: JH0798; MUID:93040225

A:Accession: JH0798

A:Molecule type: mRNA

A:Residues: 1-730 <KOI>

A:Cross-references: GB:L00709; NID:g160844; PID:g160845

A:Experimental source: embryo

C:Comment: This protein plays a role in growth cone guidance in the developing centra

C:Keywords: glycoprotein; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-730/Product: fasciclin IV #status predicted <MAT>

F:23-627/Domain: extracellular #status predicted <EXT>

F:628-652/Domain: transmembrane #status predicted <TM>

F:653-730/Domain: intracellular #status predicted <INT>

F:44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 30.6%; Score 53; DB 2; Length 730;

Matches 13; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

OY 1 FLACEKERDLFKLILKKEDEL--GDRSIMFTYONED 34

Db 41 FLGNESHKHDFKLEKDHNSLWGARIVYNISLRD 76

RESULT 6

S55181
hypothetical protein YJL131C - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein J0682

C:Species: *Saccharomyces cerevisiae*

C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-Oct-1999

C:Accession: S55181; S05768; S56913; S71666; FQ0003

R:Katsoulou, C.; Tzermia, M.; Alexandraki, D.

submitted to the EMBL Data Library, May 1995

A:Description: The complete sequence of a 40.7 kb segment located on the left arm of

yeast hypothetical proteins.

A:Reference number: S55159

A:Accession: S55181

A:Molecule type: DNA

A:Residues: 1-356 <KAT>

A:Cross-references: EMBL:X87371; NID:g854542; PIDN:CAA60824.1; PID:g854565

R:Souciet, J.L.; Nagy, M.; le Gouar, M.; Lacroute, F.; Potier, S.

Gene 79, 59-70, 1989

A:Title: Organization of the yeast URA2 gene: identification of a defective dihydroor

A:Reference number: S05766; MUID:89378778

A:Accession: S05768

A:Molecule type: DNA

A:Residues: 1-124 <SOU>

A:Cross-references: EMBL:M27174

R:Katsoulou, C.; Tzermia, M.; Alexandraki, D.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56912

A:Accession: S56913

A:Molecule type: DNA

A:Residues: 1-356 <KAW>

A:Cross-references: EMBL:249406; NID:g1008333; PIDN:CAA60824.1; PID:g1008334; MIPS:YJ

R:Katsoulou, C.; Tzermia, M.; Tavernarakis, N.; Alexandraki, D.

Yeast 12, 787-797, 1996

A:Title: Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome

of chromosome XI.

A:Reference number: S71666

A:Accession: S71666

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-356 <KAF>

A:Cross-references: EMBL:X87371; NID:g854542; PIDN:CAA60824.1; PID:g854565

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995

C:Genetics:

A:Map position: 10L

Query Match 30.3%; Score 52.5; DB 2; Length 356;

Best Local Similarity 33.3%; Pred. No. 17;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:15:54 ; Search time 40.26 Seconds
(without alignments)
32.699 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173
Sequence: 1 FLACERKDLFLKKEDELGRSIFMTYONED 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	100.0	193	IL18_HUMAN	014116 homo sapien
2	141	80.5	193	IL18_HORSE	09xsg7 equus cabal
3	139	81.3	192	IL18_PIG	019073 sus scrofa
4	134	77.5	193	IL18_CANFA	09xsr0 canis fam11
5	131	75.7	193	IL18_BOVIN	09tu73 bos taurus
6	123	71.1	192	IL18_MOUSE	P70380 mus musculu
7	119	68.8	194	IL18_RAT	P97366 rattus norv
8	58	33.5	522	AOE_ONCMY	P49253 oncorhynch
9	53.5	30.9	1359	ATRX_CAEEL	09u760 caenorhabdi
10	53	30.6	259	DNA_BP72	P12427 bacterioph
11	53	30.6	730	SM1A_SCHAM	Q26473 schistocerc
12	52.5	30.3	101	S107_BOVIN	Q28050 bos taurus
13	52.5	30.3	356	YJN1_YEAST	P47015 saccharomyc
14	52	30.1	1277	YMW6_YEAST	Q04264 saccharomyc
15	51.5	29.8	432	ENO_SYNY3	P77972 synecocyst
16	51.5	29.8	2262	RRLP_P12HT	P26676 human parai
17	51	29.5	307	XYEL_PSEPU	P06622 pseudomonas
18	49.5	28.6	231	RECO_COXBU	P51838 coxiella bu
19	49	28.3	93	S10A_BOVIN	P02639 bos taurus
20	49	28.3	93	S10A_RAT	P35467 rattus norv
21	49	28.3	307	XYLE_PSEAR	P27887 pseudomonas
22	49	28.3	399	LOJC_BOCAI	P57382 buchnera ap
23	49	28.3	1195	LYK6_YEAST	P36168 saccharomyc
24	48.5	28.3	1459	GEA2_YEAST	P39993 saccharomyc
25	48.5	28.0	124	Y729_METUA	O58139 methanococc
26	48.5	28.0	474	DLDH_HAIYO	O04829 halobacteri
27	48	27.7	93	S10A_MOUSE	P55565 mus musculu
28	48	27.7	150	SP2A_STRPU	P44110 strongyloce
29	48	27.7	190	VA52_VACCV	Q01220 vaccinia vi
30	48	27.7	307	NAHI_PSEPU	P08127 pseudomonas
31	48	27.7	326	RNHL_SCHPO	O10236 schizosacch
32	48	27.7	468	FIIB_BOVIN	P02676 bos taurus
33	48	27.7	546	SVR_THEME	O9x0h8 thermotoga

34	48	27.7	632	1	PABP_DROME	P21187 drosophila
35	47.5	27.5	400	1	INRP_BOVIN	P21327 bos taurus
36	47	27.2	75	1	DMS2_PACDA	O93452 pachymedusa
37	47	27.2	93	1	DNA_HUMAN	P23297 homo sapien
38	47	27.2	259	1	DNA_BP74	P04392 bacterioph
39	47	27.2	336	1	SIFA_SALTY	O56061 salmoneilla
40	47	27.2	527	1	AOFA_CANFA	P56027 canis fam11
41	47	27.2	4385	1	VP73_CAEEL	O09222 caenorhabdi
42	46.5	26.9	347	1	Y806_METUA	O58216 methanococc
43	46.5	26.9	399	1	INRP_HUMAN	P49441 homo sapien
44	46.5	26.9	434	1	ENO_LOLPE	O02654 loligo peal
45	46.5	26.9	759	1	TRP1_RABIT	O9tun9 oryctolagus

ALIGNMENTS

```

RESULT 1
ID IL18_HUMAN STANDARD: PRT: 193 AA.
AC 014116: 075599;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interleukin-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
DE IL18 OR IGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micaleff M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein."
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RN SEQUENCE FROM N.A.
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18."
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human Interleukin 18 cDNA."
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 2-193 FROM N.A.
RA Conti B., Kim S.-J., Tinti C., Chun H.-S., Joh T.H.;
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN - FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
RN AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
RN CELLS.
RN - SUBCELLULAR LOCATION: Secreted.
RN - SIMILARITY: BELONGS TO THE IL-18 FAMILY.
-----
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EMBL: D49950; BAA08706.1; -.
EMBL: AF077611; AAC27787.1; -.

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DR EMBL: AY044641; AAK95950.1; -
 DR EMBL: U90434; AAB50010.1; -
 DR MIM: 600953; -
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SO SEQUENCE 193 AA; 22326 MW; 323C62C20378BD55 CRC64;

Query Match 100.0%; Score 173; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.3e-15;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACKEKRDLFKLTKKEDELGDRSIMFTYONED 34
 DB 160 FLACKEKRDLFKLTKKEDELGDRSIMFTYONED 193

RESULT 2
 ID IL18_HORSE STANDARD; PRT; 193 AA.
 AC Q9XS07; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 OS IL18 OR IGIF.
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nicolas L., Penha-Goncalves M.N., Keanle J.L., Logan N.A.,
 RA Argyle D.J., Onions D.E.;
 RT "Nucleotide sequence of equine Interleukin 12 and 18 cDNAs";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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 CC -----
 DR EMBL: Y11131; CAA72013.1; -
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 SO SEQUENCE 193 AA; 22058 MW; 4D81535E904ECAP CRC64;

Query Match 81.5%; Score 141; DB 1; Length 193;
 Best Local Similarity 76.5%; Pred. No. 1.8e-11;
 Matches 26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLACKEKRDLFKLTKKEDELGDRSIMFTYONED 34
 DB 160 FLACKEKRDLFKLTKKEDELGDRSIMFTYONED 193

RESULT 3
 ID IL18_PIG STANDARD; PRT; 192 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 OS IL18 OR IGIF.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Foss D.L., Murlaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muneta Y., Mori Y.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=20260994; PubMed=10803849;
 RA Fourout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
 RA Oswald E., Oswald I.P.;
 RT "Cloning, chromosomal location, and tissue expression of the gene for
 RT pig interleukin-18";
 RL Immunogenetics 51:358-365(2000).
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U68701; AAC18415.1; -
 DR EMBL: AB010003; BAA24135.1; -
 DR EMBL: AF191088; BAF71200.1; -
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SO SEQUENCE 192 AA; 22026 MW; 8B1EA654E221A17A CRC64;

Query Match 80.3%; Score 139; DB 1; Length 192;
 Best Local Similarity 76.5%; Pred. No. 3.3e-11;
 Matches 26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLACKEKRDLFKLTKKEDELGDRSIMFTYONED 34
 DB 159 FLACKEKRDLFKLTKKEDELGDRSIMFTYONED 192

RESULT 4
 ID IL18_CANFA STANDARD; PRT; 193 AA.
 AC Q9XS07; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:15:01 ; Search time 105.02 Seconds

(without alignments)
56.007 Million cell updates/sec

Title: US-09-780-035-71

Sequence: 1 FLACEKERDLFKLIKKEDELGDRSIMFTYQVED 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	97.7	193	4	096KJ8
2	166	96.0	193	6	09BGT5
3	147	85.0	192	6	09BGT5
4	131	75.7	178	6	09BGT5
5	128	74.0	192	6	09BGT5
6	128	74.0	193	6	09BGT5
7	108	62.4	196	11	09BGT5
8	65.5	37.9	198	13	09BGT5
9	62	35.8	211	13	09BGT5
10	59	34.1	314	2	09BGT5
11	55.5	32.1	1055	4	09BGT5
12	52.5	30.3	270	11	09BGT5
13	52.5	30.3	391	2	09BGT5
14	52.5	30.3	506	11	09BGT5
15	52	30.1	590	16	09A146
16	51.5	29.8	1119	10	004390

17	51.5	29.8	1689	12	0991H9	0991H9 crimean-con
18	51.5	29.8	1689	12	091W14	091W14 crimean-con
19	51.5	29.8	1689	12	0911R1	0911R1 crimean-con
20	51	29.5	307	2	09L780	09L780 pseudomonas
21	51	29.5	307	2	09L780	09L780 pseudomonas
22	51	29.5	347	3	09HFS3	09HFS3 pneumocysti
23	51	29.5	354	16	P94583	P94583 bacillus su
24	51	29.5	357	16	099V00	099V00 staphylococ
25	51	29.5	431	16	099V00	099V00 staphylococ
26	51	29.5	590	2	054525	054525 streptococ
27	51	29.5	1066	4	096538	096538 homo sapien
28	50.5	29.2	384	16	09PMX1	09PMX1 campylobact
29	50.5	29.2	388	2	09P9F3	09P9F3 campylobact
30	50.5	29.2	1684	12	066034	066034 crimean-con
31	50	28.9	195	16	051524	051524 botreilia bu
32	50	28.9	258	16	025120	025120 helicobacte
33	50	28.9	258	16	09ZM95	09ZM95 helicobacte
34	50	28.9	314	2	09EXM0	09EXM0 escherichia
35	50	28.9	314	2	09EXM0	09EXM0 escherichia
36	50	28.9	314	2	09ZAN5	09ZAN5 pseudomonas
37	50	28.9	643	10	09SL99	09SL99 arabidopsis
38	50	28.9	807	2	09EYK2	09EYK2 streptococ
39	50	28.9	3944	5	018667	018667 caenorhabdi
40	49.5	28.6	196	2	09ZNF1	09ZNF1 escherichia
41	49.5	28.6	208	3	096VW8	096VW8 cryptococcu
42	49.5	28.6	642	3	09HEW4	09HEW4 cryptococcu
43	49.5	28.6	847	4	09NUC1	09NUC1 homo sapien
44	49.5	28.6	905	4	014700	014700 homo sapien
45	49	28.3	158	2	09RPA1	09RPA1 salmonella

ALIGNMENTS

RESULT 1
ID 096KJ8 PRELIMINARY: PRT: 193 AA.
AC 096KJ8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jiaxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF380360; AAK57024.1;
SQ SEQUENCE 193 AA: 22323 MW: 28500205D187E5F7 CRC64;

Query Match 97.7%, Score 169, DB 4; Length 193;
Best Local Similarity 97.1%, Pred. No. 1,4e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 FLACEKERDLFKLIKKEDELGDRSIMFTYQVED 34
DB 160 FLACEKERDLFKLIKKEDELGDRSIMFTYQVED 193
RESULT 2
ID 09BGT5 PRELIMINARY: PRT: 193 AA.
AC 09BGT5:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18.
GN IL18.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21229850; PubMed=11331040;
 RA Clivedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
 Hodara V.L.,
 "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
 RT Simian Immunodeficiency Virus Does Not Result in Increased Viral
 RT Replication."
 RL J. Interferon Cytokine Res. 21:173-180(2001).
 DR EMBL: AF303732; AAK13416.1;
 SO SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;

Query Match 96.0%; Score 166; DB 6; Length 193;
 Best Local Similarity 94.1%; Pred. No. 3,6e-15;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVONED 34
 DB 160 FLACEKERDLFKLLKKDELDGDSIMFTVONED 193

RESULT 3
 ID 095M33 PRELIMINARY; PRT; 192 AA.
 AC 095M33;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERFERON-GAMMA INDUCING FACTOR.
 GN IGIF.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hanlon L., McGillivray C.P., Argyile D.J.A., Nicolson L., Onions D.E.;
 RT "Nucleotide sequence of feline IGIF cDNA (provisional).";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y13923; CAC42918.1;
 SO SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 85.0%; Score 147; DB 6; Length 192;
 Best Local Similarity 82.4%; Pred. No. 1,5e-12;
 Matches 28; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVONED 34
 DB 159 FLACEKERDLFKLLKKDELDGDSIMFTVONEN 192

RESULT 4
 ID 09MZ18 PRELIMINARY; PRT; 178 AA.
 AC 09MZ18;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERLEUKIN-18 (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY, LIVER, BLOOD MONONUCLEAR CELLS;
 RA Olsen S.C., Lee I.K., Wang S.M., Kehrl M., Bolin C.A.;
 RT "Cloning of bovine Interleukin-18, expression in Escherichia coli, and
 RT characterization of the biologic activities of the recombinant
 RT cytokine."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF173175; AAF89833.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 FT NON_TER 178 178
 SO SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 75.7%; Score 131; DB 6; Length 178;
 Best Local Similarity 70.6%; Pred. No. 2,3e-10;
 Matches 24; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVONED 34
 DB 145 FLACEKERDLFKLLKKDDNRKDSVMTVONON 178

RESULT 5
 ID 09N1P7 PRELIMINARY; PRT; 192 AA.
 AC 09N1P7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERLEUKIN-18.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RX MEDLINE=20356335; PubMed=10901174;
 RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;
 RT "Cloning, sequencing, and expression of porcine Interleukin-18 in
 RT Escherichia coli."
 RL Mol. Cells 10:343-347(2000).
 DR EMBL: AF176949; AAF35169.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1
 SO SEQUENCE 192 AA; 21969 MW; A51EB7AAE221A16D CRC64;

Query Match 74.0%; Score 128; DB 6; Length 192;
 Best Local Similarity 70.6%; Pred. No. 6,3e-10;
 Matches 24; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVONED 34
 DB 159 FLACEKERDLFKLLKKDELDGDSIMFTVOSKN 192

RESULT 6
 ID 09GL09 PRELIMINARY; PRT; 193 AA.
 AC 09GL09;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERLEUKIN-18 (IGIF).
 GN IL-18.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:03:37 ; Search time 39.04 Seconds
(without alignments)
21.272 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173

Sequence: 1 FLACEKERDLFKLIKKEDELGRSIFVTYONED 34

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued Patents_AA:*
2: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	100.0	157	2	US-08-896-605A-6
2	173	100.0	157	2	US-08-896-501A-4
3	173	100.0	157	2	US-08-884-324-1
4	173	100.0	157	3	US-08-996-338-26
5	173	100.0	157	4	US-08-558-818-1
6	173	100.0	157	4	US-08-974-469A-1
7	173	100.0	157	4	US-08-832-180-1
8	173	100.0	157	4	US-08-832-198-6
9	173	100.0	157	2	US-08-896-605A-2
10	173	100.0	157	2	US-08-896-501A-2
11	173	100.0	157	2	US-08-832-180-9
12	173	100.0	157	2	US-08-502-535B-2
13	173	100.0	157	2	US-08-908-005A-2
14	173	100.0	157	3	US-08-996-338-27
15	173	100.0	157	4	US-08-558-818-7
16	173	100.0	157	4	US-08-974-469A-7
17	173	100.0	157	4	US-08-832-180-8
18	173	100.0	157	4	US-08-832-198-11
19	173	100.0	157	4	US-08-253-523-2
20	173	100.0	157	4	US-09-251-911-2
21	173	100.0	157	1	US-08-121-713D-58
22	173	100.0	157	1	US-08-835-268-58
23	173	100.0	157	3	US-09-060-692-58
24	173	100.0	157	3	US-08-833-391-58
25	173	100.0	157	3	US-09-060-610-58
26	173	100.0	157	5	PCR-US94-10151A-58
27	173	100.0	157	4	US-08-832-198-3

28	50	28.9	244	3	US-08-750-145A-24	Sequence 24, Appl
29	50	28.9	244	3	US-08-975-698A-28	Sequence 28, Appl
30	50	28.9	244	4	US-09-417-090-28	Sequence 28, Appl
31	50	28.9	244	4	US-09-727-578-28	Sequence 28, Appl
32	47	27.2	312	1	US-08-247-908A-2	Sequence 2, Appl
33	47	27.2	312	1	US-08-453-942-2	Sequence 2, Appl
34	47	27.2	312	2	US-08-926-885A-2	Sequence 2, Appl
35	47	27.2	312	5	PCR-US94-05280-2	Sequence 2, Appl
36	47	27.2	751	3	US-08-946-026-6	Sequence 6, Appl
37	46	26.6	331	4	US-09-413-231-4	Sequence 4, Appl
38	45	26.0	1089	1	US-08-180-195-36	Sequence 36, Appl
39	45	26.0	1089	1	US-08-168-917-4	Sequence 36, Appl
40	45	26.0	1089	1	US-08-477-329-36	Sequence 36, Appl
41	45	26.0	1089	2	US-08-475-458-36	Sequence 36, Appl
42	45	26.0	1089	2	US-08-460-510-4	Sequence 4, Appl
43	45	26.0	1089	2	US-08-460-490-4	Sequence 4, Appl
44	45	26.0	1089	3	US-08-980-400-36	Sequence 36, Appl
45	45	26.0	1089	3	US-08-462-728-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-6
Sequence 6, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 July 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-6

Query Match 100.0%; Score 173; DB 2; Length 157;
Best local Similarity 100.0%; Pred. No. 1,5e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACERDLEKLLKKEDELGDSIMFTYQND 34
Db 124 FLACERDLEKLLKKEDELGDSIMFTYQND 157

RESULT 2
US-08-896-501A-4
Sequence 4, Application US/08896501A
Patent No. 5891663

GENERAL INFORMATION:

APPLICANT: TANIMOTO, Tadao

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/896,501A

FILING DATE: 18-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 213,267/1996

FILING DATE: 25-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 31,474/1997

FILING DATE: 31-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TANIMOTO-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-896-501A-4

Query Match 100.0%; Score 173; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACERDLEKLLKKEDELGDSIMFTYQND 34

Db 124 FLACERDLEKLLKKEDELGDSIMFTYQND 157

RESULT 3
US-08-884-324-1
Sequence 1, Application US/08884324
Patent No. 6060283

GENERAL INFORMATION:

APPLICANT: TAKANOI, OKURA

APPLICANT: KAKUJI, TORIGOE

APPLICANT: MASASHI, KURIMOTO

TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/884,324

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 185,305/96

FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKURA-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-884-324-1

Query Match 100.0%; Score 173; DB 3; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACERDLEKLLKKEDELGDSIMFTYQND 34

Db 124 FLACERDLEKLLKKEDELGDSIMFTYQND 157

RESULT 4

US-08-996-338-26

Sequence 26, Application US/08996338

Patent No. 6087116

GENERAL INFORMATION:

APPLICANT: TORIGOE, KAKUJI

APPLICANT: OKURA, Takao

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,338

FILING DATE: 22-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74,697/1997

FILING DATE: 12-MAR-1997

PRIOR APPLICATION DATA: